



Wed Jan 30 11:57:36 2002

us-09-722-838-2.fst

Page 2

seq\_name: gb\_est1:AA788343  
seq\_documentation\_block: 363 bp mRNA EST 31-JUL-1998  
LOCUS AA788343.1 Aspergillus nidulans 24hr asexual developmental and  
DEFINITION vegetative cDNA lambda zap library Emericella nidulans cDNA clone  
r7c08a1 5', mRNA sequence.  
ACCESSION AA788343 GI:2848574  
VERSION AA788343.1  
KEYWORDS EST.  
SOURCE Emericella nidulans.  
ORGANISM Emericella nidulans; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Eukaryota; Fungi; Ascomycota; Emericella.  
REFERENCE 1 (bases 1 to 363) Hausner, J., Lai, H., Martin, W., Aramayo, R.,  
Kupfer, D., Gray, J., Prade, R. and Roe, B.  
TITLE An Aspergillus nidulans EST Database  
JOURNAL Unpublished (1998)  
COMMENT Other: Bruce A. Roe, University of Oklahoma, broeou.edu  
Department Center for Chemistry and Biochemistry, University of Oklahoma  
Advanced Center for Genome Technology, University of Oklahoma  
620 Parrington Oval, Norman, OK 73019, USA  
Tel: 405 325 4912  
Fax: 405 325 7762  
Email: broeou.edu  
We anticipate the future release of the cDNA clones to the Fungal  
Genetics Stock Center  
Seq primer: SK  
High quality sequence stop: 319.  
Location/Qualifiers  
FEATURES  
Source  
1.363  
/organism="Emericella nidulans"  
/strain="PGSC A26"  
/db\_xref="taxon:162425"  
/clone="r7c08a1"  
/clone\_lib="Aspergillus nidulans 24hr asexual  
developmental and vegetative cDNA lambda zap library"  
/note="Vegetative mycelia, asexual structures;  
developmental and vegetative mycelia, asexual structures;  
tissue type: vegetative mycelia, asexual structures;  
note: Vector: pBluescript SK-; Site 1: EcoRI; Site 2:  
XhoI; 5' end of cDNA cloned into XhoI site of pBluescript"  
3' end of cDNA cloned into XhoI site of pBluescript"  
BASE COUNT 98 a 97 c 79 g 89 t  
ORIGIN  
alignment\_scores: 322.50 Length: 91  
Quality: 3.839 Gaps: 1  
Ratio: 92.308 Percent Identity: 67.033  
Percent Similarity:  
alignment\_block:  
us-09-722-838-2 x AA788343  
Align seg 1/1 to AA788343 from: 1 to: 363

seq\_name: gb\_est2:BG810102  
seq\_documentation\_block: 651 bp mRNA EST 22-MAY-2001  
LOCUS BG810102 Magnaporthe grisea Appressorium Stage cDNA  
DEFINITION mgct002xn09f Magnaporthe grisea cDNA clone mgct002xn09f 5', mRNA sequence.  
ACCESSION BG810102 GI:14181082  
VERSION BG810102.1  
KEYWORDS EST.  
SOURCE Magnaporthe grisea.  
ORGANISM Magnaporthe grisea; Ascomycota; Pezizomycotina; Sordariomycetes;  
Eukaryota; Fungi; Ascomycota; Magnaporthe.  
REFERENCE 1 (bases 1 to 651)  
TITLE Chou, W. and Dean, R.A.  
JOURNAL Construction and sequence analysis of an appressorium stage cDNA  
COMMENT Library in the rice blast fungus, Magnaporthe grisea  
Unpublished (2001)  
CONTACT: Ralph A. Dean  
Fungal Genomics Laboratory  
North Carolina State University  
Campus Box 7251, Raleigh, NC 27695, USA  
Tel: 919-513-0020  
Fax: 919-513-0024  
Email: ralph.dean@ncsu.edu  
Seq primer: T3 primer (ATTACCCCTCAAGGCG).  
Location/Qualifiers  
FEATURES  
Source  
1.651  
/organism="Magnaporthe grisea"  
/strain="70-15"  
/db\_xref="taxon:148305"  
/clone="mgct002xn09f"  
/clone\_lib="Magnaporthe grisea Appressorium Stage cDNA"  
/dev\_stage="Germinated conidia on appressorium-inductive  
surface"  
/note="Vector: pBluescript SK(+) Vector; Site 1: EcoRI;  
Site 2: XhoI; The appressorium formation germinated for 5-8 hr  
library was constructed from conidia germinated over 55,000  
on an inductive surface. The library contains over 1.5 kbp."  
clones with average insert size of 1.5 kbp."  
BASE COUNT 152 a 193 c 159 g 147 t  
ORIGIN  
alignment\_scores: 321.50 Length: 151  
Quality: 2.679 Gaps: 4  
Ratio: 79.470 Percent Identity: 43.709  
Percent Similarity:

alignment\_block:  
US-09-722-838-2 x BG810102 ..

Align seg 1/1 to: BG810102 from: 1 to: 651

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5 SerGlyValSerIleAlaAspGluCysIleThrAlaPheAsnAspPheAr 21
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
209 TCCGAGACCAACCGCTCGCAGAGAGTGGCTGACGACGACGACGACGAC 258
21 GmetSerGlyAsnLysAlaAsnLysThrLysPheIleIlePheLysIleA 38
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
259 GCTCGGCAAGAAC.....ATCAAGTACATCATCTTCAAGCTCT 296
38 laaAspAsnLysGluValValIleAspGluValSerGluGluLysP 54
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
297 CAGCAACAACAAAGAGATTGTGGTGGAGAGCGCTCGGCGACTCCGAC 346
55 TyrGluValPheArgSerArgLeu.....GluAlaThrLysAspSerLy 69
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
347 TGGGAGAACTTCCGCAACACACTGTCTCAACCTCAACCTCAAGTCCCA 396
69 sGly.....AsnProAlaProArgTyrAlaValTyrAspValGluTyr 84
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
397 TGGTGTGTGTGGCAAGGCTCCCGCTACGCGCTACGACCTTCCAGTACA 446
84 sPLeuGlyGlyGlyGlyGlyLysArgSerLysIleValPheIleSerTrp 100
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447 CCGGCGCTTCGGGAGAGGTGACGGAACAAGATTACTTATTGCGCTGG 496
101 ValProSerAspThrProThrLeuTrpSerMetIleTyrAlaSerThrAr 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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117 gLuAsnLeuLysAsnAlaLeuAsn...IleHisThrSerIleHisAlaA 133
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133 sPaAspLysGlyAspIleGluTrpLysThrValIleAlaGluAlaSerLy 149
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150 Gly 150
|||
647 GGC 649

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seq\_name: gb\_est2:BG809838

seq\_documentation\_block: 652 bp mRNA EST 22-MAY-2001  
LOCUS BG809838  
DEFINITION mgc001x116f Magnaporthe grisea Appressorium Stage cDNA Magnaporthe  
grisea cDNA clone mgc001x116f 5', mRNA sequence.

ACCESSION BG809838  
VERSION BG809838.1 GI:14180818  
KEYWORDS EST.  
SOURCE Magnaporthe grisea.  
ORGANISM Magnaporthe grisea  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes Incertae sedis; Magnaportheaceae; Magnaporthe.

REFERENCE 1 (bases 1 to 652)  
AUTHORS Choi, W. and Dean, R.A.  
TITLE Construction and sequence analysis of an appressorium stage cDNA  
JOURNAL library in the rice blast fungus, Magnaporthe grisea  
COMMENT unpublished (2001)  
Contact: Ralph A. Dean  
Fungal Genomics Laboratory  
North Carolina State University  
Campus Box 7251, Raleigh, NC 27695, USA  
Tel: 919-513-0020  
Fax: 919-513-0024  
Email: ralph\_dean@ncsu.edu  
Seq primer: T3 primer (AATTAACCTCACTAAGG).

FEATURES

Location/Qualifiers

source

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1. .652
/organism="Magnaporthe grisea"
/strain="70-15"
/db_xref="taxon:148305"
/clone="mgc001x116f"
/clone_1b="Magnaporthe grisea Appressorium Stage cDNA"
/dev_stage="germinated conidia on appressorium-inductive
surface"
/note="Vector: pBluescript SK(+). Vector, site 1: EcoRI;
site 2: XhoI. The appressorium formation-specific cDNA
library was constructed from conidia germinated for 5-8 hr
on an inductive surface. The library contains over 55,000
clones with average insert size of 1.5 kbp."
BASE COUNT 152 a 193 c 160 g 147 t
ORIGIN

```

alignment\_scores:

```

Quality: 321.50 Length: 151
Ratio: 2.679 Gaps: 4
Percent Similarity: 79.470 Percent Identity: 43.709

```

alignment\_block:

US-09-722-838-2 x BG809838 ..

Align seg 1/1 to: BG809838 from: 1 to: 652

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5 SerGlyValSerIleAlaAspGluCysIleThrAlaPheAsnAspPheAr 21
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
208 TCCGAGACCAACCGCTCGCAGAGAGTGGCTGACGACGACGACGAC 257
21 GmetSerGlyAsnLysAlaAsnLysThrLysPheIleIlePheLysIleA 38
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
258 GCTCGGCAAGAAC.....ATCAAGTACATCATCTTCAAGCTCT 295
38 laaAspAsnLysGluValValIleAspGluValSerGluGluLysP 54
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
296 CAGCAACAACAAAGAGATTGTGGTGGAGAGCGCTCGGCGACACTCCGAC 345
296 CAGCAACAACAAAGAGATTGTGGTGGAGAGCGCTCGGCGACACTCCGAC 345
55 TyrGluValPheArgSerArgLeu.....GluAlaThrLysAspSerLy 69
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
346 TGGGAGAACTTCCGCAACACACTGTCTCAACGCCAAGATGATCTACGCC 395
69 sGly.....AsnProAlaProArgTyrAlaValTyrAspValGluTyr 84
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
396 TGGTGTGTGTGGCAAGGCTCCCGCTACGCGCTACGACCTTCCAGTACA 445
84 sPLeuGlyGlyGlyGlyGlyLysArgSerLysIleValPheIleSerTrp 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
446 CCGTGGCTTCGGGAGAGGTGACGGAACAAGATTACTTATTGCGCTGG 495
101 ValProSerAspThrProThrLeuTrpSerMetIleTyrAlaSerThrAr 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
496 TCTCTGATGACGCTGTGTCTCAACGCCAAGATGATCTACGCCGCTCCA 545
117 gLuAsnLeuLysAsnAlaLeuAsn...IleHisThrSerIleHisAlaA 133
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
546 GGACGCTCTTAAGCGCGCCCTGACGCGCATGCCACGACACTGCAAGCCA 595
133 sPaAspLysGlyAspIleGluTrpLysThrValIleAlaGluAlaSerLy 149
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
596 ACGAGCGCGGACGACATCGAATACACTCTGTCTGAGAACGCTCAGCAAG 645
150 Gly 150
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646 GGC 648

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seq\_name: gb\_est1:AL386255

seq\_documentation\_block: 500 bp mRNA EST 03-AUG-2000  
LOCUS AL386255  
DEFINITION M8C33E06F1 MtBC Medicago truncatula cDNA clone M8C33E06 T3, mRNA  
sequence.

(bases 1 to 500)  
 Jouneau, E. P., Crespeau, H., van 't Hulzen, D., Gouzy, J.,  
 Huelber, A., Carreau, V., Chataigner, O., Kahn, D., Gianfranceschi, P.,  
 V. and Gamas, P.  
 Medicago truncatula ESTs from endomycorrhizal roots  
 Unpublished (2000)  
 Contact: Genoscope  
 Genoscope - Centre National de Séquençage  
 BP 191 91006 Evry cedex - France  
 Email: [secre@genoscope.cns.fr](mailto:secre@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
 Contact : Pascal Gamas and Etienne-Pascal Jouneau, Laboratoire d'  
 Biologie Moléculaire des Relations plantes-Microorganismes,  
 CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email :  
[Etienne.Pascal.Jouneau@inra.fr](mailto:Etienne.Pascal.Jouneau@inra.fr),  
[WebSite@inra.fr](mailto:WebSite@inra.fr))  
 M-est@toulouse.inra.fr  
<http://sequence.toulouse.inra.fr/Mtruncatula.html>  
 Location/Qualifiers

```
1..500
/organism="Medicago truncatula"
/cultivar="Jema long"
/db_xref="taxon:3880"
/clone="MEBC33E06"
/clone_lib="MTBC"
/clone_type="vaccinaria inoculation with Glomus"
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alignment_scores:	253.50	Length:	149
Quality:	305	Gaps:	4
		+	34,899

alignment\_block: AL386255

1 MetalaleuAlaSerGlyValIsc...  
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[illegible]

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      34 lephelyllealaaspasnlkysglguvalvallyleakspgluValSer 164
          ::::::::::::::::::::|
      115 TGRIRAGCTTGATGACACTCAACAATCGCTTAAAGAAGTGTT 67
          ::::::::::::::::::::|
      51 gInglugluAspTYrGIuValPhearGeSrIrgluAlaThrLysAs 209
          ::::::::::::::::::::|
      165 GAGGAAGCTACTTATGACGACTTATTAAGTACTACTCAAGT..... 84
          ::::::::::::::::::::|
      67 pserlysglyasnproalaproargtyralavalryraspyalgutyrA 243
          ::::::::::::::::::::|
      210 .....GCRCCTGGTCGTACGCTTTATGATTTCACATfAg 100
          ::::::::::::::::::::|
      84 spleuglyglylglygluLylysargserlysllevalPheileSerTrp 290
          ::::::::::::::::::::|
      244 AA...AAGCCGGTAGAGCTCAACGTACAGATCGCATTCACCTGG 117
          ::::::::::::::::::::|
      101 ValProSerAsprhnProthrleuTrpsemetleleryAlaSerThrAr 340
          ::::::::::::::::::::|
      291 ATACCGATGATGCCAAGTCACAGACACAAAAGCTTACCTTCACAGCAA 133
          ::::::::::::::::::::|
      117 ggluasnleu..LysaaAlaleuasnliehtsrserllshisAlaA 390
          ::::::::::::::::::::|
      341 GGACGCTATTCGCACAGACTGTGAGCGCTTGCCATCCAATTAACAGAAC 148
          ::::::::::::::::::::|
      133 spAsplysglyAspIIegIurtplysthyrhvallleuAlaGluaIsEr 437
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seq_name: qD_esi1.AL386256

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FEATURES  
source

on: block: 544 bp mRNA  
 866256 AC33E06F1 MtBC Medicago truncatula cDNA clone MTBC33E06 T7, mRNA  
 386256 386256  
 386256.1 GI:3686007  
 trical medic.  
 trunatula  
 karyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 permatophyta; Magnoliophyta; eudicotyledons: core eudicots;  
 rosidae: eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;  
 medicago.  
 (bases 1 to 544)  
 ount: E.P., Crespeau, H., van Tuinen, D., Gouzy, J., Jallion, O.,  
 iblel, A., Carreau, V., Chataigner, O., Kahn, D., Gianfranceschi-Pearson  
 V. and Gamas, P.  
 Medicago truncatula ESTs from endomycorrhizal roots  
 unpublished (2000)  
 Medicago  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 Evry cedex - France  
 Email: segrat@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 Contact : Pascal Gamas and Etienne Pascal Journet, Laboratoire de  
 Biologie Moleculaire des Relations Plantes-Microorganismes,  
 CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email :  
 Mt-est@tolouse.inra.fr Website :  
 http://sequence.tolouse.inra.fr/Mttruncatula.html).  
 location, Toulouse, Toulousiers



root fragments colonized by the arbuscular mycorrhizal fungus *Glomus intraradices* (Schenck & Smith, isolate LP48). The plants were watered every day and twice a week with a modified nutrient Long Ashton solution without phosphate but with a high level of nitrate. After 3 weeks RNA was extracted from whole root systems. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into Uni-zap XR vector from Stratagene and packaged using GigaPack Gold packaging extracts. Plasmids containing cDNA inserts were mass-excised from phage stocks using ExsacII helper phage and propagated in SOLR cells. Clone ordering and sequencing was performed by the Centre National de Sequençage (Genoscope, Evry, France). Note : EST may be of fungal origin."

BASE COUNT 173 a 91 c 98 g 182 t  
ORIGIN

alignment\_scores:  
Quality: 253.50 Length: 149  
Ratio: 2.305 Gaps: 4  
Percent Similarity: 73.826 Percent Identity: 34.899

alignment\_block:  
US-09-722-838-2 x AL386256 ..

Align seg 1/1 to: AL386256 from: 1 to: 544

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18 AGCTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTC 67
   |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:
17 eAsnAspPheArgMetSerGlyAlaAsnGlyAlaAsnGlyAlaAsnGly 34
   |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:
68 TCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTC 105
   |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:
34 LePheValIleAlaAspAsnGlyValGluValAlaIleAspGluValSer 50
   |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:
106 TGTATAGCTTCATGATGATGATGATGATGATGATGATGATGATGATGAT 155
   |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:
51 GInGluGluAspTyrGluValPheArgSerArgLeuGluAlaThrLysAs 67
   |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:
156 GAAGAAGCTACTTATGACGACTTATGACGACTTATGACGACTTATGACG 200
   |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:
67 PserLysGlyAsnProAlaProArgTyrAlaValTyrAspValGluTyrA 84
   |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:
201 .....GGTCCCTGCTTACGCTGTTATGATTCGACTATG 234
   |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:
84 sPLeuGlyGlyGluGluGlyLysArgSerLysIleValPheIleSerTrp 100
   |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:
235 AA...AAGCCCGGTGAAGGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 281
   |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:
101 ValProSerAspThrProThrLeuTrpSerMetIleTyrAlaSerThrAr 117
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282 ATACCTGATGATTCGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 331
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117 GcLysAsnLeu...LysAsnAlaLeuAsnIleHisThrSerIleHisAla 133
   |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:
332 GGCAGCTATTCGCAAGAGACTGTCGCTGCTGCTGCTGCTGCTGCTGCT 381
   |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:
133 sPAspLysGlyAspIleGluTyrPheThrValLeuAlaGluAlaSer 148
   |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:
382 CAGATTATCCGAGGTTTCTTATGAAAGCTGACTGAAAAAGCTTCT 428

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seq\_name: gb\_est2:BI190659

seq\_documentation\_block:

LOCUS BI190659 431 bp mRNA EST 10-JUN-2001

DEFINITION 13809fs.r1 Fusarium sporotrichioides Tr1 10 overexpressed cDNA

ACCESSION BI190659  
VERSION BI190659.1 GI:14664338

KEYWORDS EST.  
SOURCE Fusarium sporotrichioides.  
ORGANISM Fusarium sporotrichioides.

REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; mitosporic Hypocreales; Fusarium.  
1 (bases 1 to 431)  
Ren,Q., Tag,A., Peglow,A., Lal,H., Kupfer,C., Peterson,A., Beremand M. and Roe,B.

TITLE Analysis of a Fusarium sporotrichioides EST database  
JOURNAL Unpublished (2001)  
CONTACT: Bruce A. Roe, University of Oklahoma, broe@ou.edu  
Department of Chemistry and Biochemistry  
Advanced Center for Genome Technology, University of Oklahoma  
620 Parrington Oval, Norman, OK 73019, USA  
Tel: 405 325 4912  
Fax: 405 325 7762  
Email: broe@ou.edu

Contact Dr. Marian Beremand regarding clone availability. Included is the best homolog from a blastx search of Genbank nr 04-09-01 336 3e-31 g111276984|p1r1|T49 cot11n related protein (imported) -Neuros  
Seq primer: T3  
High quality sequence stop: 397.

#### FEATURES

##### source

1..431  
/organism="Fusarium sporotrichioides"  
/strain="Tr1 10"  
/db\_xref="taxon:5514"  
/clone="13809fs"  
/clone\_1ib="Fusarium sporotrichioides Tr1 10 overexpressed cDNA library"  
/note="vector: pBluescript SK-; site\_1: EcoRI; site\_2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript ; 3' end of cDNA cloned into XhoI site of pBluescript"  
BASE COUNT 105 a 135 c 91 g 100 t  
ORIGIN

alignment\_scores:  
Quality: 251.00 Length: 114  
Ratio: 2.728 Gaps: 3  
Percent Similarity: 80.702 Percent Identity: 43.860

alignment\_block:  
US-09-722-838-2 x BI190659 ..

Align seg 1/1 to: BI190659 from: 1 to: 431

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5 SerGlyValSerIleAlaAspGluCysIleThrAlaPheAsnAspPheAr 21
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100 TCCGAGCCACCGCTTCCGAGCTGCTATTCGCTATTCGCTATTCGCTATTC 149
   |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:
21 gMetSerGlyAsnLysAlaAsnLysThrLysPheIleIlePheLysIleA 38
   |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:
150 GCTTAC.....AAGAAGTCAAGTTCATGCTGCTCAAGCTCT 187
   |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:
38 IaAspAsnLysGluValAlaIleAspGluValSerGInGluGluAsp 54
   |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:
188 CTGACGCTCAAGAGATGTTGTCGAGAAAGCTTCGAGAGCAAGAGAG 237
   |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:
55 TyrGluValPheArgSerArgLeu...GluAlaThrLysAspSerLysG 70
   |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:
238 TGGGAGAGCTTCGCTGAGAGCTTCGCTACGCTTACCTCCAGAGCAAAAC 287
   |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:
70 Y.....AsnProAlaProArgTyrAlaValTyrAspValGluTyrA 84
   |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:
288 TGGCAGCGTTCGCAAGGCTCCCGCTTACGCCGTTTACGATTCGAGTACA 337
   |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:
84 sPLeuGlyGlyGluGluGlyLysArgSerLysIleValPheIleSerTrp 100
   |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:
338 ACCTGCTCTGCGGATGATCCGAAACAAGATCACCTTCATCGCTGG 387
   |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:
101 ValProSerAspThrProThrLeuTrpSerMetIleTyrAla 114

```



5 SerGlyValSerIleAlaAspGluCysIleThrAlaPheAsnAspPheAr 21  
 |||||  
 60 TCTGGAGTTCAGGTCGACCCCGAGGCGGAGGCTTTCGACAACTG.. 107  
 21 gmetSerGlyAsnIysAlaAsnIysThrLysPheIleIlePheLysIleA 38  
 |||||  
 108 .....ATGTCCTGACAGCTCAGGTACATCATCTCAAGCTTT 144  
 38 IaAspAsnIysLysGluValValIleAspGluValSerGln.....Glu 52  
 |||||  
 145 CGGACGAGCTTCAGAGATGTCTATTGAGACACCAAGGAGGCCGCCACC 194  
 53 GluAspTyrGluValPheArgSerArgLeu.....GluAlaThrLysAs 67  
 |||||  
 195 GAGAACTACGACGAGATCCCGAGAAAGCTCTCAACGCCCACTAAGAG 244  
 67 pSerLysGly.....AsnProAlaProArgTyrAlaValTyrAspValG 82  
 |||||  
 245 CGCTTCTGGCCCATCAGCAAGGGTCCCGATATGCGTCTACGATTTCG 294  
 82 IuTyrAspLeuGlyGlyGlyLysArgSerLysIleValPheIle 98  
 |||||  
 295 AGTACAACTTCGCTGCTGCGAGGGTCCCGCAACAGGTGACCTTATC 344  
 99 SerTyrValProSerAspThrProThrLeuTrpSerMetIleTyrAla 115  
 |||||  
 345 GCCTGTGCTCCCGATGATGCTGCGATCAAGTCCAAAGATGCTACGCC 394  
 115 rThrArg 117  
 |||||  
 395 TTCCAAG 401

seq\_name: gb\_est1:AM710227

seq\_documentation\_block:

LOCUS AM710227 394 bp mRNA EST 25-APR-2000  
 DEFINITION e2b10ne.f1 Neurospora crassa evening cDNA library Neurospora crassa  
 CDNA clone e2b10ne 5', mRNA sequence.

ACCESSION AM710227  
 VERSION AM710227.1 GI:7599311

KEYWORDS EST.  
 SOURCE Neurospora crassa.  
 ORGANISM Neurospora crassa

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Sordariales; Sordariaceae; Neurospora.

REFERENCE 1 (bases 1 to 394)  
 AUTHORS Zhu,H., Lai,H., Kupfer,D., Dunlap,J.C. and Roe,B.A.

TITLE Two Neurospora crassa EST Databases

JOURNAL Unpublished (1998)

COMMENT Contact: Bruce A. Roe, University of Oklahoma, broeou.edu  
 Department of Chemistry and Biochemistry  
 Advanced Center for Genome Technology, University of Oklahoma  
 620 Parrington Oval, Norman, OK 73019, USA  
 Tel: 405 325 4912  
 Fax: 405 325 7762  
 Email: broeou.edu

We anticipate the future release of the cDNA clones to the Fungal  
 Genetics Stock Center  
 Seq primer: Universal Forward Primer  
 High quality sequence stop: 356.

FEATURES  
 source

1..394  
 Location/Qualifiers

/organism="Neurospora crassa"  
 /strain="Strain 30-7 (bd; A)"  
 /db\_xref="taxon:5141"

/clone="e2b10ne"

/clone\_lib="Neurospora crassa evening cDNA library"  
 /tissue\_type="tissue harvested following 22hr growth in  
 dark"

/note="Vector: pBluescript SK-; Site\_1: XbaI; Site\_2:  
 EcoRI; See: Bell-Pedersen,D., et al. PNAS 93:13096,1996.  
 5' end of cDNA cloned into XbaI site of pBluescript; 3'  
 end of cDNA cloned into EcoRI site of pBluescript"

BASE COUNT 96 a 117 c 97 g 84 t  
 ORIGIN

alignment\_scores:  
 Quality: 218.50 Length: 116  
 Ratio: 2.571 Gaps: 4  
 Percent Similarity: 73.276 Percent Identity: 40.517

alignment\_block:  
 us-09-722-838-2 x AM710227

Align seg 1/1 to: AM710227 from: 1 to: 394

5 SerGlyValSerIleAlaAspGluCysIleThrAlaPheAsnAspPheAr 21  
 |||||  
 60 TCTGGAGTTCAGGTCGACCCCGAGGCGGAGGCTTTCGACAACTG.. 107  
 21 gmetSerGlyAsnIysAlaAsnIysThrLysPheIleIlePheLysIleA 38  
 |||||  
 108 .....ATGTCCTGACAGCTCAGGTACATCATCTCAAGCTTT 144  
 38 IaAspAsnIysLysGluValValIleAspGluValSerGln.....Glu 52  
 |||||  
 145 CGGACGAGCTTCAGAGATGTCTATTGAGACACCAAGGAGGCCGCCACC 194  
 53 GluAspTyrGluValPheArgSerArgLeu.....GluAlaThrLysAs 67  
 |||||  
 195 GAGAACTACGACGAGATCCCGAGAAAGCTCTCAACGCCCACTAAGAG 244  
 67 pSerLysGly.....AsnProAlaProArgTyrAlaValTyrAspValG 82  
 |||||  
 245 CGCTTCTGGCCCATCAGCAAGGGTCCCGATATGCGTCTACGATTTCG 294  
 82 IuTyrAspLeuGlyGlyGlyLysArgSerLysIleValPheIle 98  
 |||||  
 295 AGTACAACTTCGCTGCTGCGAGGGTCCCGCAACAGGTGACCTTATC 344  
 99 SerTyrValProSerAspThrProThrLeuTrpSerMetIleTyrAla 114  
 |||||  
 345 GCCTGTGCTCCCGATGATGCTGCGATCAAGTCCAAAGATGCTACGCC 392

seq\_name: gb\_est1:AM444327

seq\_documentation\_block:

LOCUS AM444327 544 bp mRNA EST 25-SEP-2000  
 DEFINITION AB292 Primordium cDNA library Agaricus bisporus cDNA 5' similar to  
 Coffilin, mRNA sequence.

ACCESSION AM444327  
 VERSION AM444327.1 GI:10282125

KEYWORDS EST.  
 SOURCE Agaricus bisporus.  
 ORGANISM Agaricus bisporus

Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
 Agaricales; Agaricaceae; Agaricus.

REFERENCE 1 (bases 1 to 544)  
 AUTHORS Ospina-Giraldo,M.D., Collopy,P.D., Romaine,C.P. and Roysse,D.J.

TITLE Classification of sequences expressed during the primordial and  
 basidiome stages of the cultivated mushroom Agaricus bisporus

JOURNAL Fungal Genet. Biol. 29 (2), 81-94 (2000)

COMMENT Contact: Manuel D. Ospina-Giraldo  
 Mushroom Research Laboratory, Department of Plant Pathology  
 The Pennsylvania State University  
 305 Buckhout, University Park, PA 16802, USA  
 Tel: 8148633073  
 Fax: 8148637217  
 Email: mxo11@psu.edu

Seq primer: T7.

FEATURES  
 source

1..544  
 Location/Qualifiers

/organism="Agaricus bisporus"  
 /strain="Sylvan-130"

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BASE COUNT
ORIGIN
151 a 121 c 130 g 142 t
    /db_xref="taxon:5341"
    /clone_lib="Primordium CDNA library"
    /clone_lib="Primordium"
    /tissue_type="Primordium"
    /note="Vector: pBluescript II SK (+); Site_1: SalI;
    Site_2: NotI"

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alignment_scores:      Length: 149
                       Gaps: 4
                       Quality: 1.946
                       Rmalty: 74.497
Percent Similarity:    Percent Identity: 30.201

alignment_block:      ..
US-09-722-838-2 x AW444327
..
from: 1 to: 544

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US-09-722-836-2  
Align seg 1/1 to: AM444327 from: 1 to: 544  
GluValSerIleLeuAspGlycSerIleThrAlaPheAsnAs 19

[illegible]

seq\_name: gb\_ests1:BF422360  
EST  
28-NOV-2000  
req\_documentation\_block: 725 bp mRNA  
LOCUS BF422360 Earthworm lambda zap Express Library Lumb  
ACACIA ACTOPHORIN,  
DEFINITION Lr\_ad\_16 5' similar to sp|P37167|ACFP  
CDNA clone Lr\_ad\_16 5' similar to sp|P37167|ACFP  
mRNA sequence.  
EST  
BF422380.1 GI:11410369  
Accession  
Version  
Keywords  
Source  
Organism  
REFERENCE  
AUTHORS  
TITLE  
Expressed sequence tags from the humus earthworm L. rubellus

unpublished 2000)  
 Contact: Sturzenbaum SR  
 School of Biosciences  
 Cardiff University  
 PO Box 911, Biomedical Building, Museum Avenue, Cardiff, CF10 3US  
 UK  
 Tel: +44 2920 874119  
 Fax: +44 2920 874094  
 Email: sturzenbaum@cardiff.ac.uk  
 Seq primer: T3 sequencing primer  
 High quality sequence stop 490.  
 Location/Qualifiers

```

FEATURES
source
1. .725
/organism="Lumbricus rubellus"
/organism="Lumbricus 35632"

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Source
/orig.xref="taxon:35632-
/db.xref="r.ad.16"
/clone.lib="Earthworm Lambda zap Express Library"
/clone.lib="Whole worm"
/tissue_type="adult"
/dev_stage="adult"
/note="Vector: pBK-CMV; The library was prepared using
protocol given by supplier (Stratagene)."
205 a 150 c 179 g 191 t
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alignment_scores:	210.00	length:	144
quality:	2.079	gaps:	5
ratio:	70.139	percent identity:	31.944
percent similarity:			

```
alignment_block: ..
ms-09-722-838-2 x BF422380
```

```

Align seg 1/1 to: BF22280 from: 1
3 LeuAlaSerGlyValSerIleAlaAspGluGlySerIleThrAlaPheAsnAs 19
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
81 ATGGCACTCGGGTCGGCGGTTCACCGCTGATTCACAAACAAATATTCACGA 130
19 pheArgMetSerGlyAsnLysAlaAsnLysThrLysPheIleIlePheL 36
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
131 CATTAACCTT.....GGTCCAAAGTCCGATCATCATCGTCTACT 168
36 ysIleAlaAspAsnLysLysGluVal...ValIleAspGluValSerGln 51
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
169 CTTCTAACCGACAGACCTCAGCAGATCAGGTTACTGAAGACGCTCCACCT 218
52 GluGluAspTyrGluValPheArgSerArgLeuGluValArgThrLysAsp 68
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
219 GCGCGCTTTAGACGACTT.....GGGAGGATCTGAAGAGCG 259
68 rlyGlyAsnProAlaProArgTyrAlaValLysPheValGluTyrAspL 85
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
260 GAGACATTAAGACAAATGTCGATNGGATGGATTTGCGATCGATCTACT 309
85 euGluGlyGluGluGlyLysArgSerLysIleValPheIleSerTyrAl 101
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
310 TGGGTCAGTGACAG...CAGCGCAGCAACGCTGGCTTTTCTCGTAGCT 356
102 ProSerAspThrProThrIleTyrPheTyrSerMetIleTyrAlaSerThrArgL 118
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
357 CCGGAAATGCGCGACGGTGAACAAACAAAATGCTCTACGAGTAGACAGA 406
118 uAsnLeuLysAsnAlaLeu...AsnIleHisThrSerIleIleAlaAsp 134
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
407 TCGGTTGAAGAACTCCGCTGCGATGGCAATGGCGTAAGAGAAATCCAAAGCTCGC 456
134 sPlyGlyAspIleGluTyrPlyThrValLys 144
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
457 ACTACGCTGAATTTGGCGGTGTCAGATGTCATG 488
seq_name: gb_est1.AW708738

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seq_documentation_block:
LOCUS      AM708738      381 bp      mRNA      EST      25-APR-2000
DEFINITION c8g05ne.f1 Neurospora crassa evening cDNA library Neurospora crassa
            cDNA clone c8g05ne 5', mRNA sequence.
ACCESSION  AM708738
VERSION     AM708738.1 GI:7597787
KEYWORDS    EST.
SOURCE      Neurospora crassa.
            Neurospora crassa.
ORGANISM    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariales; Sordariaceae; Neurospora.
REFERENCE   1 (bases 1 to 381)
AUTHORS     Zhu,H., Lai,H., Kupfer,D., Dunlap,J.C. and Roe,B.A.
TITLE       Two Neurospora crassa EST Databases
JOURNAL     Unpublished (1998)
COMMENT     Contact: Bruce A. Roe, University of Oklahoma, broeseu.edu
            Department of Chemistry and Biochemistry
            Advanced Center for Genome Technology, University of Oklahoma
            620 Parrington Oval, Norman, OK 73019, USA
            Tel: 405 325 4912
            Fax: 405 325 7762
            Email: broeseu.edu
            We anticipate the future release of the cDNA clones to the Fungal
            Genetics Stock Center
            Seq primer: Universal Forward Primer
            High quality sequence stop: 198.

FEATURES
    source
        location/Qualifiers
            1..381
            /organism="Neurospora crassa"
            /strain="Strain 30-7 (bd; A)"
            /db_xref="taxon:5141"
            /clone="c8g05ne"
            /clone_1lb="Neurospora crassa evening cDNA library"
            /tissue-type="tissue harvested following 22hr growth in
            dark"
            /note="Vector: pBluescript SK-; Site 1: XbaI; Site 2:
            EcoRI; See: Bell-Pedersen,D., et al. PNAS 93:13096,1996.
            5' end of cDNA cloned into XbaI site of pBluescript; 3'
            end of cDNA cloned into EcoRI site of pBluescript"

BASE COUNT      95 a      112 c      94 g      80 t

ORIGIN
alignment_scores:
    Quality: 207.50      Length: 106
    Ratio: 2.627      Gaps: 4
    Percent Similarity: 74.528      Percent Identity: 41.509

alignment_block:
US-09-722-838-2 x AM708738 ..

Align seg 1/1 to: AM708738 from: 1 to: 381

5 SerGlyValSerIleAlaAspGluCysIleThrAlaPheAsnApphear 21
|||||
60 TCTGAGATTCAGCTGACCCGAGAGTCCGAGAGGCTTTCGACAGCTG.. 107
|||||
21 GmetSerGlyAsnLysAlaAsnLysThrLysPheIleIlePheLysIleA 38
|||||
108 .....ATGTCCTGCTCAGCTCAGTACATCTACAGACTTT 144
|||||
38 laaAspAsnLysGluValValIleAspGluValSerGln.....Glu 52
|||||
145 CGGAGACTTCAGAGAGATTCATTCATTCAGAGACACGAGAGGCGCCACC 194
|||||
53 GluAspTYrGluValPheArgSerArgLeu.....GluAlaThrLysAs 67
|||||
195 GAGAACTTCGAGAGACTCCGAGAGAGCTCGTCAACGCCAGACTTAAGAG 244
|||||
67 pSerLysGly.....AsnProAlaProArgTYrAlaValTYrAspValG 82
|||||
245 CGCTTCGCGGCATCAGCAAGAGGTCCCGATATGCCGCTACGATTTCG 294

```

```

82 lutyAspLeuGlyGlyGlyGlyLysArgSerLysIleValPheIle 98
|||||
295 AGTACAGAGCTTCGCTGTCGCGAGAGGCTTCCCGCAACAGGTGACCTTATC 344
|||||
99 SerTYrValProSerAsp 104
|||||
345 GCCTGCTCCCGCATGAT 362

seq_name: gb_est1:AM788192

seq_documentation_block:
LOCUS      AM788192      382 bp      mRNA      EST      01-MAY-2001
DEFINITION C00264-R Lambda Zap, Stratagene Blumeria graminis f. sp. hordei
            cDNA clone C00264 similar to cofillin, mRNA sequence.
ACCESSION  AM788192
VERSION     AM788192.1 GI:13899789
KEYWORDS    EST.
SOURCE      Blumeria graminis f. sp. hordei.
            Blumeria graminis f. sp. hordei.
ORGANISM    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
            Erysiphales; Erysiphaceae; Blumeria.
REFERENCE   1 (bases 1 to 382)
AUTHORS     Thomas,S.W., Rasmussen,S.W., Glaring,M.A., Rousier,J.A. and Oliver
            ,R.P.
TITLE       Gene identification in the fungal pathogen Blumeria graminis by
            expressed sequence tag analysis
JOURNAL     Unpublished (2000)
COMMENT     Contact: Rasmussen,S.W.
            Department of Yeast Genetics
            Carlsberg Laboratory
            10 Gl. Carlsbergvej, DK-2500, Copenhagen, Denmark
            Tel: 45 3327 5230
            Fax: 45 3327 4766
            Email: sw@erc.dk
            High quality sequence stop: 382
            POLYA-No.

FEATURES
    source
        location/Qualifiers
            1..382
            /organism="Blumeria graminis f. sp. hordei"
            /db_xref="taxon:52688"
            /clone="C00264"
            /clone_1lb="Lambda Zap, Stratagene"
            /cell_type="conidia"
            /lab_host="Hordeum vulgare"

BASE COUNT      130 a      81 c      76 g      95 t

ORIGIN
alignment_scores:
    Quality: 206.00      Length: 92
    Ratio: 2.861      Gaps: 1
    Percent Similarity: 78.261      Percent Identity: 42.391

alignment_block:
US-09-722-838-2 x AM788192 ..

Align seg 1/1 to: AM788192 from: 1 to: 382

34 IlePheLysIleAlaAspAsnLysGluValValIleAspGluValSe 50
|||||
2 ATTTCAGATGTCGACGATTCACAAAGTCCATCTTAGTGAGAGAGCCG 51
|||||
50 rGlnGluGluAspTYrGluValPheArgSerArgLeuGluAlaThrLysA 67
|||||
52 TAAATAATGAAGACTGGGATCTCCGCGAATAACTCTCAGCGCTCGTT 101
|||||
67 sPserLysGlyAsn.....ProAlaProArgTYrAlaValTYr 79
|||||
102 CTGTACAGAAAAATGCGCAGATGGCTAAAGACCGGAGATATCCATCTAC 151
|||||
80 AspValGluTYrAspLeuGlyGlyGlyGlyLysArgSerLysIleVa 96
|||||
152 GATTTCACCTACCAATTGACTGATGAGAGAGGTACAGAAATTAATTGT 201

```

```

FEATURES
source
1. 577
/organism="Triticum turgidum"
/cultivar="Tangdon-16"
/db_xref="taxon:4571"
/clone="WHE2154_B12_D24"
/clone_1ib="Triticum turgidum L. var. durum wheat"

```

whole plant cDNA library"  
/tissue\_type="All tissues"  
/dev\_stage="Different growth stages"  
/lab\_host="E. coli SOLR"  
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;  
Site\_1: EcoRI; Site\_2: XhoI; Plants were grown in a growth  
chamber at North Dakota State University (Klanian, Otto,  
Simons). Tissues collected from seven-day etiolated  
seedling leaf, stem, root and seed; leaf from plant at  
fourth leaf stage; spike from pre-anthesis through 20  
days after anthesis; flag leaf; leaf and stem tissue from  
tillers, and root. Total RNA and poly(A) RNA were  
prepared from each tissue and then pooled, a cDNA library  
was made, and the cDNA clones were in vivo excised to give  
pluscript phagemids in the TJ Close lab (Akhunov, Chn,  
Choi, Close, Fenton, Klanian, Otto, Simons, Zhang) at the  
University of California, Riverside. Plasmid DNA  
preparations and DNA sequencing were performed in the OD  
Anderson lab (all other authors)."

BASE COUNT 124 a 171 c 178 g 104 t  
ORIGIN

alignment\_scores:  
Quality: 199.50 Length: 141  
Ratio: 2.122 Gaps: 5  
Percent Similarity: 66.667 Percent Identity: 33.333

alignment\_block:  
US-09-722-838-2 x BF293720 ..

Align seg 1/1 to: BF293720 from: 1 to: 577

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5 SerGlyValSerIleAlaSpGluCysIleThrAlaPheAsnAspPheAr 21
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
87 TCTGGGTGGCGGTGACGAGAGGTGCTGAAGCGCTTCACAGAGCTGCG 136
21 GmetSerGlyAsnLysAlaAsnLysThrLysPheIleIlePheLysIleA 38
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
137 GCGGAG.....CGACACCGCGGTTCGTGGTGTACACAGATGG 174
38 laAspAsnLysGluValAlaIleAspGluValSerGlnGluAsp 54
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
175 ACGAGAGAGCGCCAGAGGTGCTGCGACAGCTC..... 209
55 TyrGluValPheArgSerArgLysGluValThrLysAspSerLysGlyAs 71
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
210 .....GGCGGCTCGACCGCACCTTCGACGACCTGGCGGC 244
71 nProAlaPro.....ArgTyrAlaValTyrAspValGluTyr. 83
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
245 GCGGATGCGCCCGCAGACGCTGCCGCTACGCGCTACACCGCGGACTTCG 294
84 .....AspLeuGlyGlyGlyGlyLysArgSerLysIleValPheIle 98
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
295 TGTGGAGAGACTCGCCGCGAGACCCCGCAGCAAGTCTTCTTCATC 344
99 SerTyrValProSerAspThrProThrLeuTyrSerMetIleTyrAlaSe 115
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
345 CACTGTGCGCGGAGTGGCGGAGCGAGGAACAGATGCTTACGCGAG 394
115 rThrArgLysAsnLeuLysAsnAlaLeuAsn...IleHisThrSerIleH 131
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
395 CTCCACGAGAGGCTCAAGAGAGCTGACGCGCTGACATGACGTGC 444
131 laAlaAspLysGlyAspIle 138
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
445 AGGCCACCGACCGCCAGCAGCTC 467

```

seq\_name: gb\_est1:BE425867  
seq\_documentation\_block: 620 bp mRNA EST 24-JUL-2000  
LOCUS BE425867

DEFINITION WHE0325\_D08\_G15S Wheat unstressed seedling shoot cDNA library  
ACCESSION BE425867  
VERSION BE425867.1 GI:9423710  
KEYWORDS EST.  
SOURCE bread wheat.  
ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae  
; Triticaceae; Triticum.  
1 (bases 1 to 620)  
REFERENCE  
AUTHORS Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han  
P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J.,  
Seaton,C.L. and Tong,J.C.  
TITLE The structure and function of the expressed portion of the wheat  
genomes  
JOURNAL Unpublished (2000)  
COMMENT Contact: Olin Anderson  
US Department of Agriculture, Agriculture Research Service, Pacific  
West Area, Western Regional Research Center  
800 Buchanan Street, Albany, CA 94710, USA  
Tel: 5105595773  
Fax: 5105595818  
Email: oanderson@wpr.usda.gov  
Sequence have been trimmed to remove vector sequence and low  
quality sequence with phred score less than 20  
Seq primer: StrataGene SK primer.  
Location/Qualifiers  
1..620  
/organism="Triticum aestivum"  
/cultivar="Chinese Spring"  
/db\_xref="taxon:4565"  
/clone="WHE0325\_D08\_G15"  
/clone\_id="Wheat unstressed seedling shoot cDNA library"  
/tissue\_type="Etiolated shoot"  
/dev\_stage="Five day old seedling"  
/lab\_host="E. coli SOLR"  
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;  
Site\_1: EcoRI; Site\_2: XhoI; Seeds were surface-sterilized  
, germinated and grown aseptically in the dark at room  
temperature on filter paper with water, nystatin and  
cefotaxime in covered crystallization dishes. Shoots were  
harvested. The tissue, total RNA, and poly(A) RNA were  
prepared, a cDNA library was made, and the cDNA clones  
were in vivo excised to give pluscript phagemids in the  
TJ Close lab (Choi, Close, Fenton) at the University of  
California, Riverside. Plasmid DNA preparations and DNA  
sequencing were performed in the OD Anderson lab (all  
other authors)."

BASE COUNT 130 a 180 c 190 g 120 t  
ORIGIN

alignment\_scores:  
Quality: 199.50 Length: 141  
Ratio: 2.122 Gaps: 5  
Percent Similarity: 66.667 Percent Identity: 33.333

alignment\_block:  
US-09-722-838-2 x BE425867 ..

Align seg 1/1 to: BE425867 from: 1 to: 620

```

5 SerGlyValSerIleAlaSpGluCysIleThrAlaPheAsnAspPheAr 21
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
92 TCCGAGTGGCGGTGACGAGAGGTGCTGAAGCGCTTCACAGAGCTGCG 141
21 GmetSerGlyAsnLysAlaAsnLysThrLysPheIleIlePheLysIleA 38
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
142 GCGGAG.....CGACACCGCGGTTCGTGGTGTACACAGATGG 179
38 laAspAsnLysGluValAlaIleAspGluValSerGlnGluAsp 54
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```





CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: NIH Intramural Sequencing Center  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov  
 Plate: LINC241 row: c column: 14  
 High quality sequence start: 25  
 High quality sequence stop: 727.  
 Location/Qualifiers

## FEATURES

source

1.1014

/organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3545029"  
 /clone\_lib="NIH\_MGC\_15"  
 /tissue\_type="adenocarcinoma cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: colon; Vector: pOTB1; Site:1: XhoI; Site:2:  
 EcoRI; CDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGACGAG(G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-CDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)"

BASE COUNT 211 a 290 c 302 g 211 t

ORIGIN

## alignment\_scores:

Quality: 193.50 Length: 168  
 Ratio: 1.775 Gaps: 7  
 Percent similarity: 64.881 Percent identity: 30.357

## alignment\_block:

US-09-722-838-2 x BE513092

Align seg 1/1 to: BE513092 from: 1 to: 1014

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1 MetAlaLeuAlaSerGlyValSerIleAlaAspGluCysIleThrAlaPh 17
  ::::::::::::::::::::|
91 TTGAGTTTGCCCTCGGTGCGTCTCTCATGTCATCAAGGTGT 140
  ::::::::::::::::::::|
17 easnsphearwmetserglyasnlysala.....AsnL 29
  ::::::::::::::::::::|
141 CACGACATGAAAGGTGCTCAAGTCTCAAGCCAGAGAGGTCGAAAGACC 190
  ::::::::::::::::::::|
29 ysrhlysphelellepheylylealaaspsnlysglyvalval 45
  ::::::::::::::::::::|
191 GCAGAGAGCGGTGCTCTTCTGCTGAGTGAAGACAGAAACATCATC 240
  ::::::::::::::::::::|
46 lleaspglu.....ValserGln.....GI 52
  ::::::::::::::::::::|
241 CTGGAGGAGGCGCAGAGATCCTGGTGGCGATGCGGCGACAGCTGTGCA 290
  ::::::::::::::::::::|
52 uclunspyrGluValPheargSerArgLeuGluAlaThrLysAspSerL 69
  ::::::::::::::::::::|
291 CGATCCCTACGCCACCTTGTCAAGATGCTG...CCAGTAAGGACTGC. 336
  ::::::::::::::::::::|
69 ysglyasnproalabroargtyralaValtyraspValglutyraspleu 85
  ::::::::::::::::::::|
337 .....CGCATGCCCTCTATGATGCAACCTATAGAGACC 369
  ::::::::::::::::::::|
86 GlyGlyGlyGlyGlyValArgSerLysIleValPheIleSerTrpValPr 102
  ::::::::::::::::::::|
370 .....AAGGAGAGCAGAGAGAGATGCTGTTTATCTTCTGGGCCCC 413
  ::::::::::::::::::::|
102 cserasphrProThrLeuTrpSerMetIleTyraIleSerThrArgGluA 119
  ::::::::::::::::::::|
414 CGAGCTGCGCCCTTAAGAGCAAAATGATTATGCCACCTCAAGAGAG 463
  ::::::::::::::::::::|
119 snLeuLysAsnAlaLeu...AsnIleHsrThrSerIleHisAlaasp 134
  ::::::::::::::::::::|
464 CCATCAAGAGAGAGAGGATCAAGCATGATTCGTAAGCAAACTGCG 513
  ::::::::::::::::::::|

```

135 LysGlyIleGluTrpLysThrValleuAlaGluAlaSerGlyGly 151  
 ::::::::::::::::::::|  
 514 TACGAGAGAGTCAAGGACCGCTGCACCTGCGCAGAGAGCTGGGGGCG 563  
 151 sAla 152  
 ::|  
 564 TGCC 567

seq.name: gb\_est1:BE442563

seq\_documentation\_block:

LOCUS BE442563 620 bp mRNA EST 25-JUL-2000  
 DEFINITION WHE1103\_D02\_H03S Wheat etiolated seedling root normalized cDNA  
 library Trilicium aestivum cDNA clone WHE1103\_D02\_H03, mRNA

ACCESSION BE442563

VERSION BE442563

KEYWORDS EST.

SOURCE bread wheat.

ORGANISM Trilicium aestivum

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae  
 1 (bases 1 to 620)AUTHORS Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han  
 P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T.,  
 Rausch,C.J., Seaton,C.B., Tong,J.C., and Zhang,D.TITLE The structure and function of the expressed portion of the wheat  
 genomes - Normalized root cDNA library

JOURNAL Unpublished (2000)

COMMENT Contact: Olin Anderson  
 US Department of Agriculture, Agriculture Research Service, Pacific  
 West Area, Western Regional Research Center  
 800 Buchanan Street, Albany, CA 94710, USA  
 Tel: 5105595773  
 Fax: 5105595818

Email: oanderson@pw.usda.gov

Sequence have been trimmed to remove vector sequence and low  
 quality sequence with phred score less than 20

Seq primer: Stratiene SK primer.

Location/Qualifiers

1. 620

/organism="Trilicium aestivum"

/cultivar="Chinese Spring"

/db\_xref="taxon:4565"

/clone="WHE1103\_D02\_H03"

/clone\_lib="Wheat etiolated seedling root normalized cDNA  
 library"

/tissue\_type="Root"

/dev\_stage="Five day Old etiolated seedling"

/lab\_host="E. coli DH10B"

/note="Vector: Lambda Uni-ZAP XR, excised phagemid  
 pBluescript SK; Site:1: EcoRI; Site:2: XhoI; Seeds were  
 surface-sterilized, germinated and grown aseptically in  
 the dark at room temperature on filter paper with water,  
 nystatin and cefotaxime in covered crystallization  
 dishes. Roots were harvested. The tissue, total RNA, and  
 poly(A) RNA were prepared, a cDNA library was made in the  
 T7 Clonase lab (Choi, Close, Fenton) at the University of  
 California, Riverside. The cDNA clones were in vivo  
 normalized to give phagescript phagmids before  
 normalization was carried out. The mass excision of  
 phagemid library and normalization were done in HT Nguyen  
 lab by D. Zhang at Texas Tech University. Normalization  
 protocol used was that of Soares. Plasmid DNA  
 preparations and DNA sequencing were performed in the OD  
 Anderson lab (all other authors)."

BASE COUNT 144 a 180 c 186 g 110 t

ORIGIN

alignment\_scores:

144 a 180 c 186 g 110 t

us-09-722-838-2.1st

Wed Jan 30 11:57:36 2002

Quality: 192.50 Length: 141  
 Ratio: 2.048 Gaps: 5  
 Percent Similarity: 66.667 Percent Identity: 31.915

alignment\_block:  
 US-09-722-838-2 x BE442563 ..

Align seg 1/1 to: BE442563 from: 1 to: 620

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5 serglvalserllealaspglucylserllethralphasnasphear 21
|||||.....:|||||.....:|||||.....:|||||.....:
105 TCCGGGTGGCGGTGATGACAGAGCTGAGTGTCCAGAGCTGCG 154
21 gmetserglvalasnlyasnllysthrlyspheillellepheylslea 38
|:::.....:|||||.....:|||||.....:|||||.....:
155 GCGCGAG.....:CGCAGCAGCGGTCTGCTGTACAGATG 192
38 laaspasnlysthrlygluvalylleaspgluvalserglnguasp 54
|||||.....:|||||.....:|||||.....:|||||.....:
193 ACACACACCCGACGAGCTGTGTGACAGAGTG.....: 227
55 tyrgluvalpheargserargluvalthralphasnasphear 71
:::|||||.....:|||||.....:|||||.....:|||||.....:
228 .....:GCGCCCTCAGCAGCTGCTGACAGCTGCTGACCTG 83
71 nproalapro.....:ArgTYAlaValTYrAspValGluTYr. 83
|||.....:|||||.....:|||||.....:|||||.....:
263 GCGATGCGCCGCGACGCTGCGCTGACGCTGCTGACAGCTGCTG 98
84 .....:Aspleuglygluvalylleaspgluvalserglnguasp 98
|||.....:|||||.....:|||||.....:|||||.....:
313 TGTCGACGACACGCGCGGAGCAGCGCGGAGCAGTCTCTCTATC 362
99 sertrypalproserasphtrprothleutrpsermettletrypalse 115
|||.....:|||||.....:|||||.....:|||||.....:
363 CACTGTCGCGCGAGCTGCTGAGCAGCGGAGCAGTCTGTAIGCCAG 412
115 tthrarggluasnlleuylasnlysthrlyspheillellepheylslea 131
|||.....:|||||.....:|||||.....:|||||.....:
413 CTCACGAGAGGCTGCTGAGAGAGCTGAGAGCTGCTGAGAGCTG 462
131 isalaspaspllysglyaspile 138
:::|||||.....:|||||.....:|||||.....:|||||.....:
463 AGCCACGACGCGCGAGCTGCTGAGAGCTGCTGAGAGCTGCTG 485

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seq\_name: gb\_est1.BE517626 EST 08-AUG-2000

seq\_documentation\_block: 548 bp mRNA  
 LOCUS BE517626  
 DEFINITION WHE0801\_H06\_O1125 wheat vernalized crown cDNA library Triticum

ACCESSION BE517626  
 VERSION BE517626.1 GI:9741656  
 KEYWORDS EST.  
 SOURCE bread wheat.  
 ORGANISM Triticum aestivum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae  
 Triticaceae; Triticum.

REFERENCE  
 AUTHORS 1 (bases 1 to 548)  
 Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han  
 P.S., Hsia, C.C., Kang, Y., Iazo, G.R., Miller, R., Rausch, C.J.,  
 Seaton, C.L. and Tong, J.C.  
 The structure and function of the expressed portion of the wheat  
 genomes - Vernalized crown cDNA library

TITLE  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Olin Anderson  
 US Department of Agriculture, Agriculture Research Service, Pacific  
 West Area, Western Regional Research Center  
 800 Buchanan Street, Albany, CA 94710, USA  
 Tel: 5105595773  
 Fax: 5105595818  
 Email: andersenpw.usda.gov

## FEATURES

source

Sequence have been trimmed to remove vector sequence and low  
 quality sequence with phred score less than 20  
 quality sequence with phred score less than 20  
 Seq primer: Stratiagene SK primer  
 location/Qualifiers

1..548  
 /organism="Triticum aestivum"  
 /cultivar="Chinese Spring"  
 /db\_xref="taxon:4565"  
 /clone="WHE0801\_H06\_O11"  
 /clone\_id="Wheat vernalized crown cDNA library"  
 /tissue\_type="Crown tissue of seedling"  
 /tissue\_stage="Five-week old seedling"  
 /dev\_stage="E. coli SOLR"  
 /lab\_host="E. coli SOLR"  
 /note="Vector: Lambda Uni-ZAP XR, excised phagemid;  
 grown at 4 C for 5 weeks. The tissue, total RNA, and  
 poly(A) RNA were prepared, a cDNA library was made,  
 the cDNA clones were in vivo excised to give phages at  
 the phagemid in the T7 Close lab (Choi, Close, Fenton)  
 the University of California, Riverside. Plasmid DNA  
 preparations and DNA sequencing were performed in the OD  
 Anderson lab (all other authors)."

## BASE COUNT

ORIGIN

99 a 168 c 186 g 95 t

alignment\_scores: 191.00 Length: 143  
 Quality: 1.969 Gaps: 6  
 Ratio: 1.969 Percent Identity: 32.168

Percent Similarity: 67.832

alignment\_block:  
 US-09-722-838-2 x BE517626 ..

Align seg 1/1 to: BE517626 from: 1 to: 548

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5 serglvalserllealaspglucylserllethralphasnasphear 21
|||||.....:|||||.....:|||||.....:|||||.....:
13 TCGGGGTGGCGGTGATGACAGAGCTGAGTGTCCAGAGCTGCG 62
21 gmetserglvalasnlyasnllysthrlyspheillellepheylslea 38
|:::.....:|||||.....:|||||.....:|||||.....:
63 C.....:GCGGCGCGCGCGAC.....:CGGTCGTGCTGTAACAGATG 100
38 laaspasnlysthrlygluvalylleaspgluvalserglnguasp 150
|||||.....:|||||.....:|||||.....:|||||.....:
101 ACACACGCGCTGACGAGCTGTGTGACAGAGCTGCTGAGAGCTG 170
54 asptyrgluvalpheargserargluvalthralphasnasphear 189
:::|||||.....:|||||.....:|||||.....:|||||.....:
151 GCGTCGACGACCTGCGCGGAGCTGCTGAGAGCTGCTGAGAGCTG 229
70 yasnproalaproargtrypalvaltyrasyvalglutryaspseugly 229
|||||.....:|||||.....:|||||.....:|||||.....:
190 .....:TCCGCTACGCGCTGCTGAGAGCTGCTGAGAGCTGCTG 279
87 .....:glygluvalylleaspgluvalserglnguasp 279
|||||.....:|||||.....:|||||.....:|||||.....:
230 ACACACGCGCGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCG 329
97 pheillesertrypalproserasphtrprothleutrpsermettle 329
|||||.....:|||||.....:|||||.....:|||||.....:
280 TTCATCTCTGCTGCGCGGAGCTGCTGAGAGCTGCTGAGAGCTG 379
113 talasertrypalproargtrypalvaltyrasyvalglutryaspse 379
|||||.....:|||||.....:|||||.....:|||||.....:
330 GCGCAGCTCCAGAGGCTGCTGAGAGCTGCTGAGAGCTGCTGAG 408
129 erllehisalaspaspllysglyaspile 138
:::|||||.....:|||||.....:|||||.....:|||||.....:
380 ACGTGACGCGACCGACCGACCGAGCTC 408

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seq\_name: gb\_est2.BF320334

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seq_documentation_block:
LOCUS      BF320334      547 bp      mRNA      EST      29-DEC-2000
DEFINITION US52905.Y1 NCI-CGAP_Mam6 Mus musculus cDNA clone IMAGE:3672728 5'
            similar to SW:COFL_MOUSE P18760 COFILIN, NON-MUSCLE ISOFORM. ;,
            mRNA sequence.
ACCESSION  BF320334
VERSION    BF320334.1  GI:11269265
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 547)
            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
JOURNAL    Contact: Robert Strausberg, Ph.D.
            Email: cgaps-remail.nih.gov
            Tissue Procurement: Jeffrey Green M.D.
            CDNA Library Preparation: Life Technologies, Inc.
            DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            Image.lnl.gov/Image/html/iresources.shtml

FEATURES             source
source
MGI:1433496
High quality sequence stop: 461.
Location/Qualifiers
1..547
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_image="IMAGE:3672728"
/clone_id="NCI-CGAP_Mam6"
/sex="female; virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site.1: SalI;
Site.2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"

BASE COUNT      146 a      133 c      155 g      113 t
ORIGIN
alignment_scores:
Quality: 190-50      Length: 166
Ratio: 1.764      Gaps: 7
Percent Similarity: 65.060      Percent Identity: 29.518

alignment_block:
US-09-722-838-2 x BF320334
Align seg 1/1 to: BF320334 from: 1 to: 547
3 LeuAlaSerGlyValSerIleAlaAspGluCysIleThrAlaPheAsnAs 19
|||||
59 AMGGCTCTGCTGCTGCTGCTCATGATGTCATCAAGTGTTCATGA 108
19 pPheArgMetSerGlyAsnLysAla.....AsnLysThrL 31
|||||
109 CATGAAGCTTCGCAAGCTTTCACACCCAGAGAACATGAAGAAACAGA 158
31 ySPheIleIlePheLysIleAlaAspAsnLysGluValValIleAsp 47
|||||
159 AGCGGCTCTCTTTTGGCTGACGTGAGACAGAAACATCATCTCGAG 208
48 Glu.....ValserGln.....GluGluAs 54
|||||

```

```

209 GAGGGCAAGCATCCTGCTAGAGATGTGGGAGACACTGTGGAGACCC 258
54 pTyrtGluValPheArgSerArgLeuCluAlaThrLysAspSerLysGlyA 71
|||||
259 CTACACCACTTTT...GGCAAGATGCTGCCAGACAAAGGACTCC..... 298
71 snProlaProlArgTyrtAlaValaTyrtAspValGluTyrtAspLeuGlyG 87
|||||
299 .....CGCTATGCACCTTATGATGACAACTATGACACC..... 331
88 GlyGluGlyLysArgSerLysIleValPheIleSerTrpValProSerAs 104
|||||
332 AAGGAGAGCAAGAGAGACCACTGCTCATCTTGTGGCCCGCAGAA 381
104 pThrProThrLeuTrpSerMetIleTyrtAlaSerThrArgLysAlaLeu 121
|||||
382 TGCACCCCTCAAGAGCAAAATGATCATCTCAGCTCCAGAGATGCCATCA 431
121 yASnAlaLeu...AsnIleHisThrSerIleHisAlaAspAspLysGly 136
|||||
432 AGAAGAGCTGACAGAGATCAAGCATGAATTTACAACTTAACTGCTACGAG 481
137 AspIleGluTrpLysThrValLeuAlaGluAlaSerGlyLysAla 152
|||||
482 GAGGTCAAGGACCGCTGCACCTGGCAGAGAAACTAGTGGCAGACGCC 529
seq_name: gb_est2:B6333134

seq_documentation_block:
LOCUS      B6333134      616 bp      mRNA      EST      27-FEB-2001
DEFINITION 602430829F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4548583 5',
            mRNA sequence.
ACCESSION  B6333134
VERSION    B6333134.1  GI:13139572
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE  1 (bases 1 to 616)
            NIH-MGC http://mgi.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
JOURNAL    Contact: Robert Strausberg, Ph.D.
            Email: cgaps-remail.nih.gov
            Tissue Procurement: DCTD/DRP/Gazdar
            CDNA Library Preparation: Ling Hong/Rubin Laboratory
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            http://Image.lnl.gov
            Plate: L12M1238 row: 1 column: 08
            High quality sequence stop: 612.
            Location/Qualifiers
1..616
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="IMAGE:4548583"
/clone_id="NIH_MGC_18"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site.1: XhoI; Site.2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH-MGC Library."

BASE COUNT      142 a      159 c      193 g      122 t
ORIGIN

```

Wed Jan 30 11:57:36 2002

us-09-722-838-2.rst

alignment\_scores: Length: 166  
Quality: 1.764 Gaps: 7  
Ratio: 1.764 Percent Identity: 30.120  
Percent Similarity: 65.060

alignment\_block:  
US-09-722-838-2 x BG333134

Align seg 1/1 to: BG333134 from: 1 to: 616

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3 leu1aserg1yvalser1le1a1sp1lucys1le1er1a1phe1a1s1n1s 19
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
111 ATGGCCCTCCGCTGCTCTCTCATGTCATGTCATCAAGGTTCACAGCA 160
19 phe1ar1metser1g1yasn1ys1a1.....Asn1ys1thr1 31
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
161 CATTGAAGTGGCTAAGTCTTCAACGCCAGAGAGGTGAAGAGCCCAAGA 210
31 ysp1he1le1le1phe1ys1le1a1a1sp1a1n1ys1l1ys1gl1val1a1le1asp 47
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
211 AGCGGCTCTCTTCTGCTGCTGAGGACAGCAAGAACATCATCTCTGAG 260
48 glu.....Valser1gn.....Glu1gn1as 54
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
261 GAGGCGCAAGAGATCCTGGTGGCGCATGTGGCCAGACTGTGCACAGACC 310
54 ptyr1gl1val1phe1ar1ser1ar1gl1eug1lual1a1thr1lys1asp1ser1ys1gl1 71
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
311 CTAGCCACACTTCTGTCAGATGCTG...TCAGATTAAGGACTGC..... 350
71 snp1ro1a1p1ro1ar1g1tyr1a1a1val1tyr1asp1a1gl1utyr1asp1leug1ly 87
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
351 .....CGCATAGCCCTCATGATGACACCTCATGAGCC..... 383
88 gly1gl1y1lys1ar1ser1ys1le1val1phe1le1ser1tr1p1a1pro1ser1as 104
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
384 AAGGAGAGCAAGAGAGATGCTGTTATCTGTCGAGCCCGCCAGATC 433
104 pth1p1ro1thr1leu1tr1p1ser1met1le1tyr1a1a1ser1thr1arg1lual1leu1 121
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
434 TGCCGCCCTTAAGCAAAATGATTATGACCGAGCTCCAGAGAGCCCATCA 483
121 yasn1ala1leu1.....Asn1le1his1thr1ser1le1his1a1a1sp1asp1ly1gl1 136
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
484 AATAAGACTGACAGAGATCAAGCATGATTCAGAACCAACTGCTACGAG 533
137 asp1le1gl1ut1r1p1ly1thr1val1leu1a1gl1ual1a1ser1gl1yl1ys1a1a 152
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
534 GAGGTCAAGAGACCCTGACACCTGTCAGAGAGAGAGCTGGGGGCGCATGCC 581
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seq\_name: gb\_ests2.BG707655

seq\_documentation\_block: 695 bp mRNA EST 07-MAY-2001  
LOCUS BG707655 602670539P1 NIH\_MGC\_96 Homo sapiens cDNA clone IMAGE:4793288 5',  
DEFINITION mRNA sequence.

ACCESSION BG707655 GI:13984217  
VERSION BG707655  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 695)  
AUTHORS NIH-MGC htlp://mgi.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-remail.nih.gov  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki  
Toshiyuki and Piero Carninci (RIKEN)

FEATURES  
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/clone\_1lb="NIH\_MGC\_96"  
/tissue\_type="hypothalamus"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: pBluescript (modified  
pBluescript KS+); Site: 1: BamHI; Site 2: SalI; XhoI (gtgag  
); Oligo-dT primed using primer 5'-TTTTTTTTTTTNN-3',  
size-selected for 5' this is a primary library enriched  
normalized to R01 5' this is a primary library  
for full-length clones and constructed using the  
Cap-trapper method (Carninci, in preparation)  
constructed by M. Brownstein (NHGRI, National  
Institutes of Health). Note: this is a NIH\_MGC Library."

BASE COUNT 148 a 187 c 223 g 137 t

ORIGIN

alignment\_scores: Length: 166  
Quality: 1.780 Gaps: 7  
Ratio: 1.780 Percent Identity: 30.120  
Percent Similarity: 64.458

alignment\_block:  
US-09-722-838-2 x BG707655

Align seg 1/1 to: BG707655 from: 1 to: 695

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3 leu1aserg1yvalser1le1a1sp1lucys1le1er1a1phe1a1s1n1s 19
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
82 ATGGCCCTCCGCTGCTCTCTCATGTCATGTCATCAAGGTTCACAGCA 131
19 phe1ar1metser1g1yasn1ys1a1.....Asn1ys1thr1 31
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
132 CATTGAAGTGGCTAAGTCTTCAACGCCAGAGAGGTGAAGAGCCCAAGA 181
31 ysp1he1le1le1phe1ys1le1a1a1sp1a1n1ys1l1ys1gl1val1a1le1asp 47
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
182 AGCGGCTCTCTTCTGCTGCTGAGGACAGCAAGAACATCATCTCTGAG 231
48 glu.....Valser1gn.....Glu1gn1as 54
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
232 GAGGCGCAAGAGATCCTGGTGGCGCATGTGGCCAGACTGTGCACAGACC 71
54 ptyr1gl1val1phe1ar1ser1ar1gl1eug1lual1a1thr1lys1asp1ser1ys1gl1 71
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
282 CTAGCCACACTTCTGTCAGATGCTG...CCAGATTAAGGACTGC..... 321
71 snp1ro1a1p1ro1ar1g1tyr1a1a1val1tyr1asp1a1gl1utyr1asp1leug1ly 87
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
322 .....CGCATAGCCCTCATGATGACACCTCATGAGCC..... 354
88 gly1gl1y1lys1ar1ser1ys1le1val1phe1le1ser1tr1p1a1pro1ser1as 104
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
355 AAGGAGAGCAAGAGAGATGCTGTTATCTGTCGAGCCCGCCAGATC 121
104 pth1p1ro1thr1leu1tr1p1ser1met1le1tyr1a1a1ser1thr1arg1lual1leu1 121
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
405 TGCCGCCCTTAAGCAAAATGATTATGACCGAGCTCCAGAGAGCCCATCA 454
121 yasn1ala1leu1.....Asn1le1his1thr1ser1le1his1a1a1sp1asp1ly1gl1 136
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
455 AATAAGACTGACAGAGATCAAGCATGATTCAGAACCAACTGCTACGAG 504
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137 AsplleGIUTrplyThrValleuAlaGluAlaSerGIyGlyAla 152
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505 GAGGTCAAGACCGCTGCACCTGCAGAGAACTGGGGGCGACGTGCC 552
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seq documentation block:
LOCUS BG447456 771 bp mRNA EST 15-MAR-2001
DEFINITION GA_Eb004303f Gossypium arboreum 7-10 dpa fiber library Gossypium
ARBOREUM CDNA clone GA_Eb004303f, mRNA sequence.
ACCESSION BG447456
VERSION BG447456.1 GI:13357108
KEYWORDS EST.
SOURCE Gossypium arboreum.
ORGANISM Gossypium arboreum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
1 (bases 1 to 771)
Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry
,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, development, and evolution
of the cotton fiber
JOURNAL Unpublished (2000)
COMMENT Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGG
High quality sequence stop: 769.
Location/Qualifiers
1. 771
/organism="Gossypium arboreum"
/strain="AKA"
/cultivar="8400"
/db_xref="taxon:29729"
/clone_lib="GA_Eb004303f"
/tissue_type="Fibers isolated from bolls harvested 7-10
dpa"
/lab_host="E. coli"
/note="Vector: PBK-CMV; Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 230 a 139 c 159 g 243 t
ORIGIN

alignment_scores:
Quality: 190.00 Length: 148
Ratio: 1.863 Gaps: 6
Percent Similarity: 68.919 Percent Identity: 31.757

alignment_block:
US-09-722-838-2 x BG447456 ..

Align seg 1/1 to: BG447456 from: 1 to: 771

4 AlaserglyValserIleAlaaspGluCysIleThrAlaPheAsnAsp 20
|||||
115 GCTTCAGGAAGGCTGTCATGATGATTCAGCAAGCTGAAGTTTAA 164
20 earGmetSerGIyAsnIlyAlaAsnIlyThr...LysPheIleIlePhe 36
: |||||
165 G.....AAGCTAAAGAGACTTACCGCTCTATATTTC 199
36 ysIleAlaAspAsnIlySerGluValIleAspGluValSerGln 52
|||||
200 AGATTGAAGAAAAAAGCAAGCAAGTCTGTGCAAAAGCTGTGAAC 249
53 GluAsp...TyrGluValPheArgSerArgIleuAlaThrIlyAsp 68

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250 ACTGATACCTATGAGCGCTTTCACCTTCAGCCGATGAG..... 294
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68 rlySGIyAsnProAlaProArgTyrAlaValTyrAspValGluTyrAsp 85
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295 .....TGTGATACCTGTGTATGACTTATTTT...G 325
85 euGIyGlyGIyGluGIyLysArgSerIlyValAlaPheIleSerIlyAl 101
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326 TGACCGATGAGAACTGCCAGAGACGAAATTTTTCATTCGCTGACT 375
102 ProSerAspTrpProThrLeuTrpSerMetIleTyrAlaSerThrArg 118
|||
376 CCTGATACATCAAAAGTAAAGCAAGATGATCTGTGAGCTCAAGGA 425
118 uAsnLeuLysAsnAlaLeuAsn...IleHisThrSerIleHisAlaAsp 134
::::
426 GAGTTCAAAAGGGAATTGATGATCAGGTGAGTGAAGCTTACCG 475
134 sPlySGIyAspIleGIUTrplyThrValleuAlaGluAlaSer 148
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476 ATCCTCCGAGATGAGATCTCGATGTCATAGAGCGCGTCCAT 519
seq_name: gb_est1:BE055736

seq documentation block:
LOCUS BE055736 817 bp mRNA EST 07-MAR-2001
DEFINITION GA_Ea003573f Gossypium arboreum 7-10 dpa fiber library Gossypium
ARBOREUM CDNA clone GA_Ea003573f, mRNA sequence.
ACCESSION BE055736
VERSION BE055736.2 GI:13246866
KEYWORDS EST.
SOURCE Gossypium arboreum.
ORGANISM Gossypium arboreum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
1 (bases 1 to 817)
Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry
,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, development, and evolution
of the cotton fiber
JOURNAL Unpublished (2000)
COMMENT On Jun 8, 2000 this sequence version replaced gl:8382793.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGG
High quality sequence stop: 808.
Location/Qualifiers
1. 817
/organism="Gossypium arboreum"
/strain="AKA"
/cultivar="8400"
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/tissue_type="Fibers isolated from bolls harvested 7-10
dpa"
/lab_host="E. coli"
/note="Vector: PBK-CMV; Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 254 a 150 c 167 g 243 t 3 others
ORIGIN

alignment_scores:
Quality: 190.00 Length: 148
Ratio: 1.863 Gaps: 6
Percent Similarity: 68.919 Percent Identity: 31.757

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Wed Jan 30 11:57:36 2002

us-09-722-838-2.lst

alignment block:  
 US-09-722-838-2 x BE055736 ..  
 Align seq 1/1 to: BE055736 from: 1 to: 817

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4 Alaserglyvalserllealaaspigucysillethralapheasnaspsh 20
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162 GCTTCAGAGAAATGCTGTCATGATGATTCAGAGTGAAGTTTGAAGACT 211
|||||.....|
20 eargmetserglyasnlyslaslnysrthr...lysphelilelephel 36
|||||.....|
212 G.....AAGCTAAAGAGACTTACCGCTTCATAGATTCA 246
|||||.....|
36 ysillealaaspasnlyslaslnysrthr...lysphelilelephel 296
|||||.....|
247 AGATTGAGAGAAACAAAGACAGATTGTCGMAAGTTGGTGAAGCT 296
|||||.....|
53 gluasp...tyrgluvalpheargserargleugluathrrlyaspse 68
|||||.....|
297 ACTGATAGCTATGAGGCTTCTACTCTAGCCTTCAGCCGATGAG.... 341
|||||.....|
342 .....TGTCGATACGCTGTGTATGATCTTGAATTT...G 372
|||||.....|
85 euglyglygluglygluysargserlysillevalphelelsertrpyal 101
|||||.....|
373 TGACCGATGAGAACTGCCAGAGAGCAGAAATTTTTCATTCCTCGTCT 422
|||||.....|
102 Proseraspthrprothrleutrpsermetlletyralaserthrargl 118
|||||.....|
423 CCTGATACATCAAAAGTAGAGAGCAAGATGATCTATGCCAGCTCAAGGA 472
|||||.....|
118 uasnleuysasnaleuasn...llelshtrserllelshlalaaspa 134
|||||.....|
473 CAGGTTCAAAAGAGAAATGATGATGATCCAGAGTTCAGAGCTACCG 522
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134 splysglyaspilleglutrpypsrthrvalleualagluasler 148
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seq\_name: gb\_est1:BE054171

seq\_documentation block: 827 bp mRNA EST 07-MAR-2001  
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 DEFINITION GA\_Ea0001D17f Gossypium arboreum 7-10 dpa fiber library Gossypium  
 arborum cDNA clone GA\_Ea0001D17f, mRNA sequence.

ACCESSION BE054171 GI:13243593  
 VERSION BE054171.2  
 KEYWORDS EST.  
 ORGANISM Gossypium arboreum.  
 Gossypium arboreum: Streptophyta; Embryophyta; Tracheophyta;  
 Eukaryota; Viridiplantae; Magnoliophyta; eudicotyledons; core eudicots;  
 Spermatophyta; Magnoliophyta; eudicotyledons; Malvaceae; Gossypium.  
 Kossidae; eucosids II; Malvales; Malvaceae; Gossypium.

REFERENCE 1 (bases 1 to 827)  
 WING, R.A., FRISCH, D., YU, Y., MAIN, D., RAMBO, T., SIMMONS, J., HENRY  
 'D', WOOD, T.C., LESLIE, A. and WILKINS, T.A.  
 An integrated analysis of the genetics, development, and evolution  
 of the cotton fiber  
 Unpublished (2000)  
 On Jun 8, 2000 this sequence version replaced gi:8381227.  
 COMMENT  
 Contact: Wing RA  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Tel: 864 656 7288  
 Fax: 864 656 4293  
 Email: rwing@clemson.edu  
 Seq primer: TAAATGAGCTCACTATAGG  
 High quality sequence stop: 692.  
 Location/Qualifiers

FEATURES

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 /organism="Gossypium arboreum"  
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 /tissue\_type="Fibers isolated from bolls harvested 7-10  
 dpa"  
 /lab\_host="E. coli"  
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 BASE COUNT 235 a 158 c 200 g 230 t 4 others  
 ORIGIN

alignment\_scores:  
 quality: 190.00 length: 148  
 ratio: 1.863 gaps: 6  
 Percent similarity: 68.919 Percent identity: 31.757

alignment block:  
 US-09-722-838-2 x BE054171 ..

Align seq 1/1 to: BE054171 from: 1 to: 827

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|||||.....|
20 eargmetserglyasnlyslaslnysrthr...lysphelilelephel 36
|||||.....|
124 G.....AAGCTAAAGAGACTTACCGCTTCATAGATTCA 158
|||||.....|
36 ysillealaaspasnlyslaslnysrthr...lysphelilelephel 208
|||||.....|
159 AGATTGAGAGAAACAAAGACAGATTGTCGMAAGTTGGTGAAGCT 208
|||||.....|
53 gluasp...tyrgluvalpheargserargleugluathrrlyaspse 68
|||||.....|
209 ACTGATAGCTATGAGGCTTCTACTCTAGCCTTCAGCCGATGAG.... 253
|||||.....|
68 rlysglyasnproalaproargtyralaValtyrAspyalglutyrAspl 85
|||||.....|
254 .....TGTCGATACGCTGTGTATGATCTTGAATTT...G 284
|||||.....|
85 euglyglygluglygluysargserlysillevalphelelsertrpyal 101
|||||.....|
285 TGACCGATGAGAACTGCCAGAGAGCAGAAATTTTTCATTCCTCGTCT 334
|||||.....|
102 Proseraspthrprothrleutrpsermetlletyralaserthrargl 118
|||||.....|
335 CCTGATACATCAAAAGTAGAGAGCAAGATGATCTATGCCAGCTCAAGGA 384
|||||.....|
118 uasnleuysasnaleuasn...llelshtrserllelshlalaaspa 134
|||||.....|
385 CAGGTTCAAAAGAGAAATGATGATGATCCAGAGTTCAGAGCTACCG 434
|||||.....|
134 splysglyaspilleglutrpypsrthrvalleualagluasler 148
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435 ATCCTTCGAGATGATGATCTGATGATCAATAGAGAGCCGCAAT 478
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seq\_name: gb\_est1:AL022775

seq\_documentation block: 551 bp mRNA EST 29-DEC-1999  
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 DEFINITION s7c19b51 Beddington mouse dissected endoderm  
 clone 528-3113 5', mRNA sequence.

ACCESSION AL022775 GI:6645348  
 VERSION AL022775.1  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus.  
 Mus musculus: Chordata; Craniata; Vertebrata; Euteleostomi;  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 551)  
 AUTHORS Harrison,S.M., Dunwoode,S.L., Arkell,R.M., Lehrach,H. and Beddington,R.S.  
 TITLE Isolation of novel tissue-specific genes from cDNA libraries representing the individual tissue constituents of the gastrulating mouse embryo  
 JOURNAL Development 121 (8), 2479-2489 (1995)  
 MEDLINE 95401865  
 COMMENT Contact: Wiles,M., Lehrach,H. and Avner,P.  
 EEC Mouse Transcript Mapping Consortium  
 Genoscope - CNS  
 2, rue Gaston Cremieux, 91000 Evry, France  
 Email: pavner@pasteur.fr  
 clone available from Ressourcenzentrum, Heubnerweg 6, D-14059 Berlin, Germany. Web site http://www.rzpd.de  
 Seq primer: CCGGTCGGGAATTCGGGGT;  
 High quality sequence only submitted.  
 Vector: pSport1; site\_1: NotI; site\_2: SalI;  
 cloned unidirectionally.  
 Dissected endoderm 7.5 days.  
 Average insert size: 1.2 kb (range: 0.2 - 2.kb).  
 Location/Qualifiers  
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 /clone="528-3113"  
 /clone\_1lb="beddington mouse dissected endoderm"  
 /tissue\_type="dissected endoderm"  
 /dev\_stage="7.5 dpc"  
 /note="Vector: pSport1; Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally. ~ High quality sequence only submitted. ~ Average insert size: 1.2 kb (range: 0.2 - 2.kb)"  
 BASE COUNT 146 a 137 c 155 g 113 t  
 ORIGIN  
 alignment\_scores:  
 Quality: 189.50 Length: 166  
 Ratio: 1.771 Gaps: 7  
 Percent Similarity: 64.458 Percent Identity: 30.120  
 alignment\_block:  
 US-09-722-838-2 x AL022775 ..  
 Align seg 1/1 to: AL022775 from: 1 to: 551  
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 78 ATGGCCTCTGGTGGCTGCTCTGATGTCATCAAGCTTTCATGA 127  
 19 pPheArGmetSerGlyAsnLysAla.....AsnLysThrL 31  
 1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 128 CATGAAGGTGCCAAGTCTTCAACACCAAGAACGAGAAACGCAAGA 177  
 31 yspHeIleIlePheLysIleAlaAspAsnLysGluValValIleasp 47  
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 178 AGCGGTGCTCTTGGCTGAGTGAAGAACATCATCTCCGAG 227  
 48 GlU.....ValSerGln.....GluGluAs 54  
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 228 GAGGGCAAGAGATCCTGTAGAGATGTGGGCGAGACTGTGACAGACC 277  
 54 pTyGluValPheArgSerArgLeuGluValThrLysAspSerLysGlyA 71  
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 278 CTCACACCACTTTTGTCAAGATGCTG...CCAGACAAAGAGACTGC..... 317  
 71 snPrcAlaPrcArgTyrAlaValTyrAspValGluTyrAspLeuGlyGly 87  
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 318 .....CGTATGCACCTATGATGACAACTATGAGACC..... 350  
 88 GlyGluGlyLysArgSerLysIleValPheIleSerTrpValProSerAs 104

351 AAGGAGCAGACAGAGAGACCGTGGTTCATCTTCTGGGCCCCGAGAA 400  
 104 pPhrProThrLeuTrpSerMetIleTyrAlaSerThrArgGluAsnLeuL 121  
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 401 TCCACCCCTCAAGAGCAAAATGATCTATGTCAGCTCCAAAGATGCCATCA 450  
 121 yAsnAlaLeu...AsnIleHisThrSerIleHisAlaAspAspLysGly 136  
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 137 AspIleGluTrpLysThrValLeuAlaGluAlaSerGlyLysAla 152  
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 seq\_documentation\_block:  
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 VERSION B1248557  
 KEYWORDS EST.  
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 Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 558)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cga@b1-remail.nih.gov  
 Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LHAM11367 row: h column: 20  
 High quality sequence start: 2  
 High quality sequence stop: 558.  
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 /tissue\_type="tumor, gross tissue"  
 /dev\_stage="7 months"  
 /lab\_host="DH10B"  
 /note="Organ: mammary; Vector: pCMV-Sport6; Site\_1: SalI; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"  
 BASE COUNT 147 a 141 c 156 g 114 t  
 ORIGIN  
 alignment\_scores:  
 Quality: 189.50 Length: 166  
 Ratio: 1.771 Gaps: 7  
 Percent Similarity: 64.458 Percent Identity: 30.120  
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 US-09-722-838-2 x B1248557 ..  
 Align seg 1/1 to: B1248557 from: 1 to: 558

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 78 ATGGCTCTGTGTGGCTGTCTGATGTCATCAAGTCTTCATCAATGA 127  
 19 pPheArgMetSerGlyValSerIleAlaAspGluCysIleThrAlaPheAsnAs 31  
 128 CATGAAGTTCGCAAGTCTTCACACCGAAGAAAGTGAAGAACCCAGAA 177  
 31 ySPheIleIlePheIleValSerIleAlaAspGluCysIleThrAlaPheAsnAs 47  
 178 AGCGGTGTCTTGTGGCTGTCTGATGTCATCAAGTCTTCATCAATGA 227  
 48 Glu.....ValSerGln.....GluGluAs 54  
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 54 pTyrgluValPheArgSerArgLeuGluAlaThrLysAspSerLysGly 71  
 278 CTACACCACTTTGTGCATGATGTCG...CCAGACCAAGAGATGTCG... 317  
 71 snProAlaProArgTyrgluValSerIleAlaAspGluCysIleThrAlaPheAsnAs 87  
 318 .....CGCTATGCACTCTATGATGCAACCTATGACAC... 350  
 88 GlyGluGlyLysArgSerLysIleValPheIleSerTrpAlaProSerAs 104  
 351 AAGAGAGACCAAGAGAGAGACCTGTGCTTCATCTCTGGGCCCCGAGAA 400  
 104 pThrProThrLeuTrpSerMetIleTyrgluValSerIleAlaAspGluCysIle 121  
 401 TGCACCCCTCAAGACCAAAATGATCTATGTCAGCTCCAGAGATGCCATCA 450  
 121 yASnAlaLeu...AsnIleHisThrSerIleHisAlaAspGluCysIle 136  
 451 AGAGAGAGCTGACAGAAATCAAGCATGATTAACAGCTAACTAGCTACGAG 500  
 137 AspIleGluTrpLysThrValLeuAlaGluAlaSerGlyIleLysAla 152  
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seq\_documentation\_block: 563 bp mRNA EST 29-APR-1997  
 LOCUS AA403518  
 DEFINITION m256all.r1 Barstead mouse pooled organs MLR44 Mus musculus cDNA,  
 clone IMAGE:717404.5, similar to gb:U00472 Mouse mRNA for cofilin,  
 complete cds and flanks (MUSE); mRNA sequence.  
 ACCESSION AA403518  
 VERSION AA403518.1 GI:2057490  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus.  
 Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 563)  
 Maier, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
 Geisler, S., Kucaba, T., Lacey, M., Le, M., Martin, J., Morris, M.,  
 Schellenberg, K., Stepien, M., Tan, F., Underwood, K., Moore, B.,  
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
 Waterston, R.  
 The Mashu-HMI Mouse EST Project  
 Unpublished (1996)  
 Contact: Marra M/Mouse EST Project  
 WashU-HMI Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1810  
 Fax: 314 286 1810  
 Email: mouseest@watson.wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 MGI:442900  
 Seq primer: -28ml3 rev2 ET from Amersham

FEATURES  
 Source Location/Qualifiers  
 1..563  
 /organism="Mus musculus"  
 /strain="FVB/N"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:717404"  
 /clone\_lib="Barstead mouse pooled organs MLR44"  
 /sex="mixed"  
 /tissue\_type="pooled organs"  
 /dev\_stage="7 day"  
 /lab\_host="DH10B"  
 /note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with  
 a modified polylinker; Site\_1: EcoRI; Site\_2: NotI; 1st  
 strand cDNA was primed with a NotI oligo(dT) primer [5']  
 3' double-stranded cDNA was ligated to Eco RI adaptors  
 (GTGGAATGCGTACC), digested with Not I and Eco RI  
 the Not I and Eco RI sites of the modified pT73 vector.  
 library constructed by Bob Barstead."

BASE COUNT 157 a 143 c 156 g 107 t  
 ORIGIN

alignment\_scores: 189.50 Length: 166  
 Quality: 1.771 Gaps: 7  
 Ratio: 64.458 Percent Identity: 30.120  
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 US-09-722-838-2 x AA403518

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 19 pPheArgMetSerGlyValSerIleAlaAspGluCysIleThrAlaPheAsnAs 31  
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 69 CATGAAGTTCGCAAGTCTTCACACCGAAGAAAGTGAAGAACCCAGAA 118  
 31 ySPheIleIlePheIleValSerIleAlaAspGluCysIleThrAlaPheAsnAs 47  
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 48 Glu.....ValSerGln.....GluGluAs 54  
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 292 AAGAGAGACCAAGAGAGAGACCTGTGCTTCATCTCTGGGCCCCGAGAA 341  
 104 pThrProThrLeuTrpSerMetIleTyrgluValSerIleAlaAspGluCysIle 121  
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 342 TGACCCCTCAAGACCAAAATGATCTATGTCAGCTCCAGAGATGCCATCA 391  
 121 yASnAlaLeu...AsnIleHisThrSerIleHisAlaAspGluCysIle 136  
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 392 AGAGAGACCTGACAGAAATCAAGCATGATTAACAGCTAACTAGCTACGAG 441  
 137 AspIleGluTrpLysThrValLeuAlaGluAlaSerGlyIleLysAla 152  
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Wed Jan 30 11:57:33 2002

us-09-722-838-2.ini

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30 rlysphelellelphelylellelaspasnllysgluvalvallea 47
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47 spgluvalsergln.....GluGluAspTyrGluValAlphe 58
179 GATCATATAGTCAGCCTTCAGATTCCTGGATAGAGATTAATGATTCCTT 228
59 ArgSerArgLeuGluAlaThrLysAspSerLysGlyAsnProAlaProAr 75
229 GTTTACCCCTGTTGAGAGCAACAA.....CCATG 260
75 gtyAlaValAlaTyrAspValGluTyrAspLeuGlyGlyGluGlyLysA 92
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92 rgseryllelevalphelisertrpvalproserasprhprothrleu 108
301 ..TAAGATGATATTCATTCATGCTCCAGATTCATTCATTCATTCGT 124
109 TrpSerMetIleTyrAlaSerThrArgGluAsnLeuLysAsnAlaLeu.. 139
349 CAAAAAATGTTGTATCCAGCACACAGACCACTCGAAGAGCAATTCG 398
125 .....AsnIleHisThrSerIleHisAlaAspAspLysGlyAspIleG 448
399 AGTGCCACATTAAGATGACATTAATTCGTCACATTCCTCC 489
139 lutrP.....LysThrValLeuAlaGluAlaSer 148
449 CATTCATGATATTAATAATCTGCTGCACATTCCTCC 489

seq_name: /cgn2_6/ptodata/2/ina/3a_COMB.seq:US-08-184-252A-1
seq_documentation_block:
  Sequence 1, Application US/08184252A
  GENERAL INFORMATION:
  APPLICANT: Beeler, John F.
  APPLICANT: Aaronson, Stuart A.
  APPLICANT: PROTEIN TYROSINE KINASE A6
  TITLE OF INVENTION: 8
  NUMBER OF SEQUENCES: 8
  CORRESPONDENCE ADDRESSES:
  ADDRESS: Knobb, Martens Olson & Bear
  STREET: 620 Newport Center Drive, Sixteenth Floor
  CITY: Newport Beach
  STATE: CA
  COUNTRY: USA
  ZIP: 92660
  COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  OPERATING SYSTEM: IBM PC compatible
  SOFTWARE: Patent Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/184,252A
  FILING DATE: 18-JAN-1994
  CLASSIFICATION: 435
  ATTORNEY/AGENT INFORMATION:
  NAME: Israelson, Ned A.
  REGISTRATION NUMBER: 29,655
  TELEPHONE: (619) 235-8550
  TELEPHONE: (619) 235-8550
  INFORMATION FOR SEQ ID NO: 1:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 3000 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
  MOLECULE TYPE: cDNA
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HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 61..1113
US-08-184-252A-1

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129 AAAGTACAGACTTCTGAAAATATCTATGTGAATAAGTACCACTTGATG 178
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59 ArgSerArgLeuGluAlaThrLysAspSerLysGlyAsnProAlaProAr 75
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125 .....AsnIleHisThrSerIleHisAlaAspAspLysGlyAspIleG 448
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seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US95-00601-1
seq_documentation_block:
  Sequence 1, Application PC/TUS9500601
  GENERAL INFORMATION:
  APPLICANT: United States of America Department of Health and Human
  APPLICANT: Services PROTEIN TYROSINE KINASE A6
  TITLE OF INVENTION: 8
  NUMBER OF SEQUENCES: 8
  CORRESPONDENCE ADDRESSES:
  ADDRESS: Knobb, Martens Olson & Bear
  STREET: 620 Newport Center Drive, Sixteenth Floor
  CITY: Newport Beach
  STATE: CA
  COUNTRY: USA
  ZIP: 92660
  COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
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47  sgluValSerGln.....GluGluAspTyrGluValPhe 58
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59  ArgSerAlaGluGluAlaThrLysAspSerLysGlysnProAlaPro 75
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seq\_name: /cgn2\_6/plodata/2/lna/5B\_COMB.seq:US-08-648-298-1

seq\_documentation\_block:

; Sequence 1, Application US/086482988  
; Patent No. 5871990

APPLICANT: HENTIK

APPLICANT: Henrik Clausen  
APPLICANT: Eric Paul Bennett  
TITLE OF INVENTION: HDD-N-3

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; TITLE OF INVENTION: UDP-N-acetyl-1-alpha-D-galactosamine:polypeptidid
; TITLE OF INVENTION: N-acetylglactosaminyltransferase GalNAc-T3

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NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:

ADDRESS: Darby & Darby PC  
STREET: 805 Third Avenue

STREET: 805 Third  
CITY: New York  
STATE: NY

STATE: NY  
ZIP: 10022

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;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Diskette

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COMPUTER: IBM PC compatible  
OPERATING SYSTEM: DOS

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7 OPERATING SYSTEM: DOS
7 SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
7 CURRENT ADDITION DATA:

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/648,298

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FILING DATE: 15-JUN-1996  
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION  
NAME: Green, Reza

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; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 4035/09866

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REFERENCE/DOCKET NUMBER: 4035/OB86;  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 2125277000  
TELEFAX: 2127536237

TELEPHONE: 212/550257  
TELEX: 236687  
INFORMATION FOR SEQ ID NO:

INFORMATION FOR SEQ ID NO:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3888 base pairs

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; LENGTH: 3889 base pairs
; TYPE: nucleic acid

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; STRANDEDNESS: double
; TOPOLOGY: linear
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MOLECULE TYPE: CDNA to mRNA  
HYPOTHETICAL: NO

; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; ORIGINAL SOURCE:

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; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens

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TISSUE TYPE: Submaxillary gland  
US-08-648-298-1

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alignment\_scores:

Quality:	75.56
Ratio:	1.302

Percent Similarity: 63.04:

alignment\_block: MS-09-722-838-2 x MS-08-648

US-09-122-838-2 X US-08-641

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Wed Jan 30 11:57:33 2002

us-09-722-838-2.rn1

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279 ACTGCTGAGCGCCGACAG.....CCCTGCTACG 307
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seq_name: /cgn2_6/ptodata/2/lna/5b_COMB.seq:us-09-123-851-2

seq_documentation_block:
Sequence 2, Application US/09123851
Patent No. 5958405
GENERAL INFORMATION:
APPLICANT: GOLI, SURYA K.
TITLE OF INVENTION: A NOVEL HUMAN PROTEIN TYROSINE KINASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
INCYTE PHARMACEUTICALS, INC.
ADDRESS: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/123-851
FILING DATE:
PRIOR APPLICATION NUMBER: 08/728,520
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0136 US
TELEPHONE: 415-845-4166
TELEFAX: 415-845-0555
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1346 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
LIBRARY:
CLONE: Consensus
US-09-123-851-2

alignment_scores:
Quality: 75.00 Length: 137
Ratio: 1.000 Gaps: 7
Percent Similarity: 54.745 Percent Identity: 24.088

alignment_block:
US-09-722-838-2 x US-09-123-851-2 ..
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seq_documentation_block:
Sequence 2, Application US/08728520
Patent No. 5994112
GENERAL INFORMATION:
APPLICANT: GOLI, SURYA K.
TITLE OF INVENTION: A NOVEL HUMAN PROTEIN TYROSINE KINASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
INCYTE PHARMACEUTICALS, INC.
ADDRESS: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,520
FILING DATE: Filed Herewith
PRIOR APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0136 US
TELEPHONE: 415-845-4166
TELEFAX: 415-845-0555
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1346 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
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LIBRARY:  
CLONE: Consensus  
US-08-728-520-2

alignment\_scores:  
Quality: 75.00 Length: 137  
Ratio: 1.000 Gaps: 7  
Percent Similarity: 54.745 Percent Identity: 24.088

alignment\_block:

US-09-722-838-2 x US-08-728-520-2 ..

Align seg 1/1 to: US-08-728-520-2 from: 1 to: 1346

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94 LysIleValPheIleSerTyrValProSerAspThrProThrLeuTyrSe 110
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446 GCCACATCA 454

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seq\_documentation\_block:

Sequence 7, Application US/08206176

Patent No. 5639940

GENERAL INFORMATION:

APPLICANT: Garner, Ian

APPLICANT: Dailymple, Michael A

APPLICANT: Prunkard, Donna E

APPLICANT: Foster, Donald C

TITLE OF INVENTION: Production of Fibrinogen in Transgenic

TITLE OF INVENTION: Animals

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: Zymogenetics, Inc.

STREET: 4225 Roosevelt Way, N.E.

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/206.176  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Parker, Gary E  
REGISTRATION NUMBER: 31-648  
REFERENCE/DOCKET NUMBER: 93-15  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-547-8080 ext 322  
TELEFAX: 206-548-2329  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10807 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: ovine beta-lactoglobulin  
US-08-206-176-7

alignment\_scores:  
Quality: 75.00 Length: 61  
Ratio: 2.206 Gaps: 1  
Percent Similarity: 55.738 Percent Identity: 32.787

alignment\_block:

US-09-722-838-2 x US-08-206-176-7/rev ..

Align seg 1/1 to reverse of: US-08-206-176-7 from: 1 to: 10807

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   ||||| :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
5006 CCGTGAATGTCACACTCTGCTGCGGAGGAGGAGGAGGAGGAGGAGGAG 4964
   ||||| :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
97 heLleSerTyrValProSerAspThrProThrLeuTyrPseMetIleTyr 113
   ||||| :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
4963 ....CAGTGGCTCTCTGCTCCACCCCGGCTGGGCGACGCCCTGAGATAC 4919
   ||||| :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
114 AlaSerThrArgGluAsnLeuLysAsnAlaLeu 124
   ||||| :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
4918 TCCCCCACTCTGCACCCCTGGGGAATGCTCTC 4886

```

seq\_name: /cgn2\_6/ptodata/2/1na/5B\_COMB.seq:US-08-756-506-5

seq\_documentation\_block:

Sequence 5, Application US/08756506

Patent No. 5905185

GENERAL INFORMATION:

APPLICANT: Garner, Ian

APPLICANT: Cottingham, Ian R.

APPLICANT: Temperley, Simon M.

APPLICANT: Foster, Donald C.

APPLICANT: Sprecher, Cindy A.

APPLICANT: Prunkard, Donna E.

TITLE OF INVENTION: PROTEIN C PRODUCTION IN TRANSGENIC

TITLE OF INVENTION: ANIMALS

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Zymogenetics, Inc.

STREET: 1201 Eastlake Avenue East

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98102



```
seq_documentation_block:
; Sequence 16, Application US/08920827
; Patent No. 5770375
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; APPLICANT: Matsuhisa, Akio
; APPLICANT: Uehara, Hirotsugu
; APPLICANT: Eda, Soji
; TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/920,827
; FILING DATE: 29-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,577
; FILING DATE: 27-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 19036/32420
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2812 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Pseudomonas aeruginosa
; STRAIN: Clinical Isolate P4-5
; US-08-920-827-16

alignment_scores:
Quality: 74.00 Length: 131
Ratio: 1.138 Gaps: 5
Percent Similarity: 49.618 Percent Identity: 19.084

alignment_block:
US-09-722-838-2 x US-08-920-827-16 ..
Align seq 1/1 to: US-08-920-827-16 from: 1 to: 2812

5 SerGlyValSerIleAlaAspGluCysIleThrAlaPheAsnAspPheAr 21
: : : : : : : : : : : : : : : : : : : : : : : : : :
847 AATCAACGGAGGTACGGCGAGCTGTATGGACCTTAACCCGTACAG 896
21 gmeSerGlyAsnLysAlaAsnLysThrLysPhe..IleIlePheLysI 37
: : : : : : : : : : : : : : : : : : : : : : : : : :
897 GCTGAGTGCAGAAAAAATGGCCGATACGCTTCGATATGTTGTCGGTG 946
37 leaIaAspAsnLysLysGluValValIleAspGluValSerGluGlu 53
: : : : : : : : : : : : : : : : : : : : : : : : : :
947 ATTATGTCATGATCAGCAAGCGCTGATCAGAAAGACC..... 984

alignment_scores:
```

```
54 AspTyrGluValPheArgSerArgLeuGluAlaThrLysAspSerLysG1 70
984 .....
70 yAsnProAlaProArgTyrAlaValTyrAspValGluTyrAspLeuGlyG 87
: : : : : : : : : : : : : : : : : : : : : : : : : :
985 .....AAATATCTTCGTATGTCATGTCATTTATTTATTTCCGTCGCG 1021
87 lYgLYglu...GlyLysArgSerLysIleValPheIleSerTyrPAlaPro 102
: : : : : : : : : : : : : : : : : : : : : : : : : :
1022 GTGGCGGATTTGTGTACGTCGATGATGATGATTTATTTCAATAT..... 1065
103 SerAspThrProThrLeuTyrPserMetIle..... 112
1066 .....TGGTGTGCTGCGCATTCGCTATGAACTTCG 1097
113 TyrAlaSerThrArgLysAsnLeuLysAsnAlaLeuAsnIle 126
: : : : : : : : : : : : : : : : : : : : : : : : : :
1098 CTATCGCAGAAAAAGATCAATGTTGCTGCTGCTGCTGCTG 1140

seq_name: /cgn2_6/ptodata/2/1na/5A_COMB.seq:US-08-921-177-16

seq_documentation_block:
; Sequence 16, Application US/08921177
; Patent No. 5798211
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; APPLICANT: Matsuhisa, Akio
; APPLICANT: Uehara, Hirotsugu
; APPLICANT: Eda, Soji
; TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/921,177
; FILING DATE: 29-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,577
; FILING DATE: 27-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 19036/32420
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2812 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Pseudomonas aeruginosa
; STRAIN: Clinical Isolate P4-5
; US-08-921-177-16

alignment_scores:
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Wed Jan 30 11:57:33 2002

Quality: 74.00 Length: 131  
Ratio: 1.138 Gaps: 5  
Percent Similarity: 49.618 Percent Identity: 19.084

Alignment block: US-09-722-838-2 x US-08-921-177-16 ..  
US-09-722-838-2 from: 1 to: 2812

Align seg 1/1 to: US-08-921-177-16 from: 1 to: 2812

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5 serglyvalserllealaaspglucysillethralapheasnsphear 21
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847 AATGCAACGCGACTGACGCGAGTGTGTATGGACTTTAACCCTACAG 896
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21 gmetserglyasnlysalasnlysnhrlysphe...lleilepelysi 37
: : : : : : : : : : : : : : : : : : : : : : : : : : :
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897 GCTGAGTGCAGAAAAAATGCGCGAATACGCTTCGATATGTTCTCGGTG 946
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: : : : : : : : : : : : : : : : : : : : : : : : : : :
37 lealaaspasnlysgluvalalleaspgluvalserglinglu 53
: : : : : : : : : : : : : : : : : : : : : : : : : : :
: : : : : : : : : : : : : : : : : : : : : : : : : : :
947 ATTATGCTCATGATCAGCAGCGCTGATCAGAGAGCC..... 984
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: : : : : : : : : : : : : : : : : : : : : : : : : : :
54 aspyrcluvlpheargserargleugluvalthrlyaspseryscl 70
: : : : : : : : : : : : : : : : : : : : : : : : : : :
: : : : : : : : : : : : : : : : : : : : : : : : : : :
984 ..... 984
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70 yasnprohlaaproargtyralavaltyraspsvalglutyraspleuglyg 87
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985 ..... 985
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87 lyglyglu...glysarargserlysllevalpheellesertrpvalpro 102
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1022 GTGGGCGAGTGTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 112
: : : : : : : : : : : : : : : : : : : : : : : : : : :
: : : : : : : : : : : : : : : : : : : : : : : : : : :
103 seraspthrprothrleutrpsermetile..... 1097
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1066 ..... 1066
: : : : : : : : : : : : : : : : : : : : : : : : : : :
113 ..tyralaserthrarglunleulysasnlealeuasnle 126
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: : : : : : : : : : : : : : : : : : : : : : : : : : :
1098 CTAATGCGCGAGAAAAAGAGTCAATGCTGCTGCTGCTGCTGCTGCTG 1140
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-362-577C-16
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seq\_documentation\_block:  
; Sequence 16, Application US/08362577C

```
; Patent No. 5807673
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; APPLICANT: Matsubisa, Akio
; APPLICANT: Uehara, Hirotsugu
; APPLICANT: Eda, Soji
; TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/362,577C
; FILING DATE: 27-Mar-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 19036/32420
```

us-09-722-838-2.rml

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448

INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2812 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
ORIGINAL SOURCE: Pseudomonas aeruginosa  
ORGANISM: Clinical isolate P4-5  
STRAIN: US-08-362-577C-16

alignment scores:  
Quality: 74.00 Length: 131  
Ratio: 1.138 Gaps: 5  
Percent Similarity: 49.618 Percent Identity: 19.084

Alignment block: US-09-722-838-2 x US-08-362-577C-16 ..  
US-09-722-838-2 from: 1 to: 2812

Align seg 1/1 to: US-08-362-577C-16 from: 1 to: 2812

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5 serglyvalserllealaaspglucysillethralapheasnsphear 21
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847 AATGCAACGCGACTGACGCGAGTGTGTATGGACTTTAACCCTACAG 896
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21 gmetserglyasnlysalasnlysnhrlysphe...lleilepelysi 37
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897 GCTGAGTGCAGAAAAAATGCGCGAATACGCTTCGATATGTTCTCGGTG 946
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37 lealaaspasnlysgluvalalleaspgluvalserglinglu 53
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947 ATTATGCTCATGATCAGCAGCGCTGATCAGAGAGCC..... 984
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54 aspyrcluvlpheargserargleugluvalthrlyaspseryscl 70
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87 lyglyglu...glysarargserlysllevalpheellesertrpvalpro 102
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1022 GTGGGCGAGTGTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 112
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103 seraspthrprothrleutrpsermetile..... 1097
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1066 ..... 1066
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113 ..tyralaserthrarglunleulysasnlealeuasnle 126
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1098 CTAATGCGCGAGAAAAAGAGTCAATGCTGCTGCTGCTGCTGCTGCTG 1140
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seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-920-828-16
```

seq\_documentation\_block:  
; Sequence 16, Application US/08920828

```
; Patent No. 5853998
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; APPLICANT: Matsubisa, Akio
; APPLICANT: Uehara, Hirotsugu
; APPLICANT: Eda, Soji
; TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
```



```

STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,828
FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Rln-Laures, Ll-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19036/32420
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Pseudomonas aeruginosa
STRAIN: Clinical Isolate P4-5
US-08-920-828-16

```

```

alignment_scores:
Quality: 74.00 Length: 131
Ratio: 1.138 Gaps: 5
Percent Similarity: 49.618 Percent Identity: 19.084

```

alignment\_block:

US-09-722-838-2 x US-08-920-828-16 ..

Align seg 1/1 to: US-08-920-828-16 from: 1 to: 2812

```

5 SerGIValSerIleAlaSPGLucysIleThrAlaPheAsnAspPheAr 21
: : : : : : : : : : : : : : : : : : : : : : : : : :
847 AATGCAAGCGAGGTGTACGGCGAGTGTGTATGGAGCTTAACCCGTACG 896
21 gmetSerGIValnLysAlaAsnLysThrLysPhe...IleIlePheLysI 37
: : : : : : : : : : : : : : : : : : : : : : : : : :
897 GCTAGTGTCAAAAAAATTGGCCGAATACGCTGCATATGCTGTCGGG 946
37 leaIAspAsnLysLysGIValValIleAspGIValSerGIValnLys 53
: : : : : : : : : : : : : : : : : : : : : : : : : :
947 AATTATGTCATGATCAGCAGCGGTGATCGAAGAAGCC..... 984
54 AspTYrGIValPheArSerArGIleuAlaThrLysAspSerLysGI 70
984 ..... 984
70 yAsnProAlaProArGIYrAlaValTYrAspValGIuTYrAspLeuGI 87
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985 .....AATATCTTCTGTATGTCTATTATTATTGCGTGGCG 1021
87 lYGIValL...GIYLYsArSerLysIleValPheIleSerTYrValPro 102
: : : : : : : : : : : : : : : : : : : : : : : : : :
1022 GTGGCGCGATGCTAAAGCTGAGTGCATCTACGATTAATTCATAT... 1065
103 SerAspThrProThrLeuTrpSerMetIle..... 112

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1066 .....TGGGTGTGCTGCGGCAATCGCTATGAACTGCG 1097
113 TYrAlaSerThrArgGIuAsnLeuLysAsnAlaLeuAsnIle 126
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1098 CTATGCGCAGAAAAAGAAAGTCAATGATGTTGTGTGCTGCTCTTG 1140

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seq\_name: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:US-08-853-948B-1

seq\_documentation\_block:

Sequence 1, Application US/08853948B

Patent No. 6210943

GENERAL INFORMATION:

APPLICANT: AKIHAMA, Toyota

TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE FROM CITRUS AND DNA ENCODING

FILE REFERENCE: 0049-0235-0

CURRENT APPLICATION NUMBER: US/08/853,948B

CURRENT FILING DATE: 1997-05-09

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 3539

TYPE: DNA

ORGANISM: Citrus unshiu

US-08-853-948B-1

alignment\_scores:

Quality: 71.50 Length: 180

Ratio: 0.794 Gaps: 10

Percent Similarity: 50.000 Percent Identity: 25.000

alignment\_block:

US-09-722-838-2 x US-08-853-948B-1 ..

Align seg 1/1 to: US-08-853-948B-1 from: 1 to: 3539

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11 AspGIuCySIIeThrAlaPheAsn.....AspPheArGIValSerGIVal 25
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25 nLYsAlaAsnLysThrLys..... 31
: : : : : : : : : : : : : : : : : : : : : : : : : :
205 TAAAGCTCAAGCAGCAGAGGAGTCTCAAGAGAGAAATACCGCGCTGACA 254
32 .....PheIleIlePheLysIleAlaAspAsnLysLysGIValVal 45
: : : : : : : : : : : : : : : : : : : : : : : : : :
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305 ...GGAGAGCGAGCTCAGAGAAATGGCGAAACGTCTGAAACGTGAAG 351
59 gSerArGIleuAlaThrLysAsp.....SerLysGIVal 71
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352 AGCGCGAGGAGGAAAGCACTGTGATATGTCTGAAGACTTGTGAGAGGAG 401
71 snProAlaProArGIYrAlaValTYrAspValGIuTYrAspLeuGI 87
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402 AAAAAGG.....GACATGTCTACGATGATGATGCGGT 433
88 ...GIYGIuGIYLYsArSerLysIleValPheIleSerTYrValPro 103
: : : : : : : : : : : : : : : : : : : : : : : : : :
434 CATGGGATGATGACTGAAAGCAGACTACCTAGAAATAGCTGCTT.... 478
103 rasPThrProThrLeuTrpSerMetIleTYrAlaSerThrArgGIValn 120
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479 .GATGCAATGAAACATGG.....ATTAGTCAACAGAAAG 512
120 eULysAsnAlaLeuAsnIleIleThrSerIleHis..... 131
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513 GAAAAAAGCTATATATTGTGTTAATAAGCATTCATCTCATACGAGGT 562

```

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132 .....Alaspsaplysglyasp1leg1ur 140
563 GAAATATGAGTGTGGCCGTGATTCATCTGCTGCTCAGGTTAGTA 612
140 plystrvalleualagualaserglyglysalaagly 153
613 TGTGTGGAAGTTCAGAGAGCTTGGGCTTCATGCCAGCA 652
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seq\_name: /cgn2\_6/prodata/2/lna/6B\_COMB.seq:us-09-073-898-144

seq\_documentation\_block:

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Sequence 144, Application US/09073898
GENERAL INFORMATION:
APPLICANT: Feltelson, Jerald S.
APPLICANT: Schnepf, H. Ernest
APPLICANT: Narva, Kenneth E.
APPLICANT: Stockhoff, Brian A.
APPLICANT: Schmeits, James
APPLICANT: Loewer, David
APPLICANT: Dullum, Charles Joseph
APPLICANT: Muller-Cohn, Judy
APPLICANT: Stamp, Lisa
APPLICANT: Morill, George
APPLICANT: Finstad-Lee, Stacey
APPLICANT: No. 6242669el Pesticidal Toxins and Nucleotide
TITLE OF INVENTION: Sequences Which Encode These Toxins
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/073,898
APPLICATION NUMBER: US/09/073,898
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-OCT-1996
PRIOR APPLICATION DATA: US 08/960,780
APPLICATION NUMBER: US 08/960,780
FILING DATE: 30-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M. 39,355
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-708C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
FAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 144:
SEQUENCE CHARACTERISTICS:
LENGTH: 1030 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-073-898-144
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alignment\_block:

US-09-722-838-2 x US-09-073-898-144

Align seg 1/1 to: US-09-073-898-144 from: 1 to: 1030

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42 sglualval.....leasglualsergling 53
514 TGAAGACGCGATACAGATGAGATTCATTCAGACATTTGGAGGAA 67
53 lualslyrglualphearsersargleualathrlaspa..... 76
564 ATGGGTATACCATC...CAAAATAGATGCGCTCAATATGAGATGATCA 610
68 .....Sertlysgly.....Asnproalaproagly 76
611 TTACGACATGAAAGGATATACGAATTTGTTCAACCCCTAGATACTCA 660
76 ralaalalyasp.....Valgluyt.....Aspleug 86
661 CACGGTGGAGATCCTTATACAGATATGAAAAAGCAGAGGAGATTAG 710
86 lylglylygllylarserserlysilvalpheliesertrpvalpro 102
711 ATTGTCAAAATGCAAAAGAAACATTAAACCCATTAGTTCGCGCTTTCCA 760
103 Serapthprrothleutrpsermetileryalasertharagluas 119
761 AGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 807
119 nleuysasnalaleusnlethsrserlethsisalaaspaaslysg 136
808 CTATCAATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 844
136 lylasplleglurp.....lystrvalleualaguala 147
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148 Serglylylalsagly 153
884 GGTGGGAGGAGCATGAGC 901
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Sequence 26, Application US/08960780
GENERAL INFORMATION:
APPLICANT: Feltelson, Jerald S.
APPLICANT: Schnepf, H. Ernest
APPLICANT: Narva, Kenneth E.
APPLICANT: Stockhoff, Brian A.
APPLICANT: Schmeits, James
APPLICANT: Loewer, David
APPLICANT: Dullum, Charles Joseph
APPLICANT: Muller-Cohn, Judy
APPLICANT: Stamp, Lisa
APPLICANT: No. 6204435el Pesticidal Toxins and Nucleotide
TITLE OF INVENTION: Sequences Which Encode These Toxins
NUMBER OF SEQUENCES: 134
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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alignment\_scores: 71.00 Length: 156  
Quality: 0.866 Gaps: 9  
Ratio: 52.564 Percent Identity: 24.359  
Percent Similarity: 52.564

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,780
FILING DATE: 30-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA-708
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-375-8100
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1278 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: 68F
US-08-960-780-26
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alignment_scores:
Quality: 71.00      Length: 156
Ratio: 0.866        Gaps: 9
Percent Similarity: 52.564      Percent Identity: 24.359
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alignment\_block:

US-09-722-838-2 x US-08-960-780-26 ..

Align seg 1/1 to: US-08-960-780-26 from: 1 to: 1278

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|||||Val.....IleAspLysValSerGlnG 53
42 sgluValVal.....IleAspLysValSerGlnG 53
514 TGAAGACACGATACAGATGAGATTCTATTCAGACATTGGGAGAGAA 563
53 LysAspTyrGluValPheArgSerArgLeuGluAlaThrLysAsp..... 67
::|||:::|||||:|||||:|||||:|||||:|||||:|||||:
564 ATGGGTATACCATC..CAAAATAGATGGCCCAATGGGATGATTCA 610
68 .....SerLysGly.....AsnProAlaProArgTyr 76
|||||:|||||:|||||:|||||:|||||:|||||:
611 TTAGCAAGTAAAGGATATACGAAATTTGTTCAAAACCACTAGATACCA 660
76 rAlaValTyrAsp.....ValGluTyr.....AspLeuG 86
:::|||||:|||||:|||||:|||||:|||||:|||||:
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86 LysGlyGlyGluGlyLysArgSerLysIleValPheIleSerTyrValPro 102
:::|||||:|||||:|||||:|||||:|||||:|||||:
711 ATTTGTCAAATGCAAAAGAAACATTAAACCATTAAGTTGGCGCTTTCCA 760
103 SerAspThrProThrLeuTyrSerMetIleTyrAlaSerThrArgGluAs 119
|||:::|||||:|||||:|||||:|||||:|||||:|||||:
761 AGCTGTAATGTGACTATGCAAAAGTGATA..TTGCTCCAGATGAGAA 807
119 nLeuLysAsnAlaLeuAsnIleHisThrSerIleHisAlaAspAspLysG 136
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808 CTTATCAAAATAGATGATCGATCTCATTCATCAGCAAT..... 844
136 LysAspIleGluTyr.....LysThrValIleuAlaGluAla 147
|||:::|||||:|||||:|||||:|||||:|||||:
845 .....TGCTGCTATACGAATACAGAGGCGCTTCATTATGAAGCT 883
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148 SerGlyGlyLysAlaGly 153
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seq\_documentation\_block:

Sequence 26, Application US/09073898

Patent No. 6242669

GENERAL INFORMATION:

APPLICANT: Feltelson, Jerald S.

APPLICANT: Schnepf, H. Ernest

APPLICANT: Narva, Kenneth E.

APPLICANT: Stockhoff, Brian A.

APPLICANT: Schmeltz, James

APPLICANT: Loewer, David

APPLICANT: Dullum, Charles Joseph

APPLICANT: Muller-Cohn, Judy

APPLICANT: Stamp, Lisa

APPLICANT: Morrill, George

APPLICANT: Finstad-Lee, Stacey

TITLE OF INVENTION: No. 6242669el Pesticidal Toxins and Nucleotide

NUMBER OF SEQUENCES: 144

CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: FL

COUNTRY: US

ZIP: 32606-6669

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/073,898

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/029,848

FILING DATE: 30-OCT-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/960,780

FILING DATE: 30-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Sanders, Jay M.

REGISTRATION NUMBER: 39,355

REFERENCE/DOCKET NUMBER: MA-708C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 352-375-8100

TELEFAX: 352-372-5800

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 1278 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: 68F

US-09-073-898-26

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alignment_scores:
Quality: 71.00      Length: 156
Ratio: 0.866        Gaps: 9
Percent Similarity: 52.564      Percent Identity: 24.359

alignment_block:
US-09-722-838-2 x US-09-073-898-26 ..
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d Jan 30 11:57:33 2002

us-09-722-838-2.rn1

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26 LysAlaAsnLysThrIlePheValIleAlaAspAsnLys 42  
464 AAAGCAACAAACAACTTACTCAAAAAGTAGAGTCTAGGA 513  
42 sgluValVal.....IleAspGluValSerGlnGlu 53  
514 TGAAACACAGATGACATGAGATTCCTATCCAGACATTTGCGAAGAAA 67  
53 LysPyrGluValPheArgSerArgGluValAlaThrLysAsp..... 610  
564 ATGGCTTACCATC...CAAAATTAAGATTGCCCAATAGGATGATTCGA 76  
68 .....SerLysGly.....AsnProAlaProArgTy 660  
611 TTACGACATAAGGATATACGAATTTGTTCAAAACCCACTAGATCTCA 86  
76 rAlaValIyrAsp.....ValGluTyr.....AspLeuG 86  
661 CACGGTTGAGATCCTTATACGATTTAGAAACAGCAGCAGGATTTAG 710  
86 LysGlyGlyGluGlyLysArgSerLysIleValPheIleSerTrpValPro 102  
711 ATTGTCAAAATGCAAAAGAAACATTATACCCATTAGTGGCGCTTTCCA 760  
103 SerAspThrProThrLeuTrpSerMetIleTyrAlaSerThrArgGluAs 119  
761 AGTGGCAATGTGAGATGCAAAAGTAGATA...TGTCTCCAGATGAGAA 807  
119 LysLysAsnAlaLeuAsnIleHisThrSerIleHisAlaAspLysG 136  
808 CTTTCAATAGTATGAGTCTCATCTCATCTAGCAAT..... 844  
136 LysAspIleGluTrp.....LysThrValLeuAlaGluAla 147  
845 .....TGATCTATACGATACGAAGGCGCTTCTATTGAAAGCT 883  
148 SerGlyGlyLysAlaGly 153  
884 GGTGGGAGACATTTAGGC 901  
seq\_name: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:US-07-721-761A-32  
seq\_documentation\_block:  
Sequence 32, Application US/07721761A  
GENERAL INFORMATION:  
PATENT NO. 5475099  
APPLICANT: Vic. C. Knauf  
TITLE OF INVENTION: Plant Fatty Acid Synthases  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS: Inc.  
STREET: 1920 Fifth Street  
CITY: Davis  
STATE: CA  
COUNTRY: USA  
ZIP: 95616  
COMPUTER READABLE FORM: Diskette, 3.50 inch, 1.0 MB  
MEDIUM TYPE: Apple Macintosh  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 6.0.7  
SOFTWARE: Microsoft Word 4.0  
CURRENT APPLICATION DATA: US/07721,761A  
FILING DATE: 19910626  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: 07/568,493  
APPLICATION NUMBER: 15-AUGUST-1990  
FILING DATE: 15-AUGUST-1990  
ATTORNEY/AGENT INFORMATION:

NAME: Elizabeth Lassen  
REGISTRATION NUMBER: 31,845  
NAME: Donna E. Scherer  
REGISTRATION NUMBER: 34,719  
REFERENCE/DOCKET NUMBER: CGNE 76-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (916) 753-6313  
TELEFAX: (916) 753-1510  
ID NO: 32:  
INFORMATION FOR SEQ. ID NO:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1533 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
US-07-721-761A-32

alignment\_scores:  
Quality: 70.50 Length: 149  
Ratio: 1.052 Gaps: 5  
Percent Similarity: 44.966 Percent Identity: 20.134

alignment\_block:  
US-09-722-838-2 x US-07-721-761A-32 from: 1 to: 1533  
Align seq 1/1 to: US-07-721-761A-32

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519 GGAAGCCCTACTACTTACTTACCAAAATGCTTATACCCCTAGATGGGTAC 79  
66 yAspSerLysGlyAsnProAlaProArgTyrAlaValTyr..... 618  
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79 .....TGACACCTGAAAGAACAGCAGCAGGATCTTCCACACCTATCTCA 668  
619 TGACACCTGAAAGAACAGCAGCAGGATCTTCCACACCTATCTCA 84  
80 .....AspValGluTyrAla 84  
669 CTTTCTGGCGGCTAGACATTTGAGCAGATACAGAACATTCAGATTC 718  
84 sPLeuGlyGlyGlyGlyLysArgSerLysIleValPheIleSerTrp 100  
719 TCATTGGGTGACGAAATGATGATCTCTGACGAA..... 750  
101 ValProSerAspThrProThrLeuTrpSerMetIleTyrAlaSerThrArg 117  
751 .....AACAGCCCTTACTT...GGTTCATCTACACATCGTTTCA 788  
117 gLysAsnLeuLysAsnAlaLeuAsnIleHisThrSerIleHisAlaAsp 134  
789 AGAGCTGACACATTTGTTTCTACGGAACACCGCCGACATGCAAGG 838  
134 sPLeuGlyAspIleGluTrpLysThrValLeuAlaGluAlaSerGly 873  
839 ATCATGGGAGCTGAAA.....CTGCCGCAAAATTTGTGCT 873  
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seq\_documentation\_block:  
Sequence 32, Application US/07978687  
GENERAL INFORMATION:  
PATENT NO. 5510255  
APPLICANT: Vic. C. Knauf  
TITLE OF INVENTION: Plant Fatty Acid Synthases  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS: Inc.  
STREET: 1920 Fifth Street  
CITY: Davis  
STATE: CA  
COUNTRY: USA  
ZIP: 95616  
COMPUTER READABLE FORM: Diskette, 3.50 inch, 1.0 MB  
MEDIUM TYPE: Apple Macintosh  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 6.0.7  
SOFTWARE: Microsoft Word 4.0  
CURRENT APPLICATION DATA: US/07978,687  
FILING DATE: 19910626  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: 07/568,493  
APPLICATION NUMBER: 15-AUGUST-1990  
FILING DATE: 15-AUGUST-1990  
ATTORNEY/AGENT INFORMATION:

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1  NUMBER OF SEQUENCES: 51
2  CORRESPONDENCE ADDRESS:
3  ADDRESSEE: Calgene, Inc.
4  STREET: 1920 Fifth Street
5  CITY: Davis
6  STATE: CA
7  COUNTRY: USA
8  ZIP: 95616
9
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
12 COMPUTER: Apple Macintosh
13 OPERATING SYSTEM: Macintosh 6.0.7
14 SOFTWARE: Microsoft Word 4.0
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER: US/07/978,687
17 FILING DATE: FEBRUARY 1, 1993
18 CLASSIFICATION: 800
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: PCT/US91/05801
21 FILING DATE: 15-AUGUST-1991
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: 07/568,493
24 FILING DATE: 15-AUGUST-1990
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: 07/721,761
27 FILING DATE: 26-JUNE-1991
28 ATTORNEY/AGENT INFORMATION:
29 NAME: Elizabeth Lassen
30 REGISTRATION NUMBER: 31,845
31 NAME: Donna E. Scherer
32 REGISTRATION NUMBER: 34,719
33 REFERENCE/DOCKET NUMBER: CGNE 76-2 WO
34 TELECOMMUNICATION INFORMATION:
35 TELEPHONE: (916) 753-6313
36 TELEFAX: (916) 753-1510
37 INFORMATION FOR SEQ ID NO: 32:
38 SEQUENCE CHARACTERISTICS:
39 LENGTH: 1533 base pairs
40 TYPE: nucleic acid
41 STRANDEDNESS: single
42 TOPOLOGY: linear
43 MOLECULE TYPE: cDNA to mRNA
44
45 US-07-978-687-32
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117 gLuunSdeutysasnaAlalaAanlleHstHrSerieslhtslAspa 134
      :|||::: ||| :::::|||||
789 AGAGCGTCCACAACTTTGTTCTCAACGGAACACGCCGACGATCAAGAG 838
134 sPLySGLyAsPtleGLuTrPlYstrHValleaJagLualaSerGly 149
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;seq_documentation_block:
;Sequence 12, Application US/08471791
; Patent No. 5723595
; GENERAL INFORMATION:
; APPLICANT: Thompson, Gregory A
; APPLICANT: Knaf, Vic C
; TITLE OF INVENTION: Plant Desaturases-Compositions
; TITLE OF INVENTION: and Uses
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: California
; COUNTRY: USA
; ZIP: 95616

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: MicrosoftWord 5.1 (a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,791
FILING DATE: 6-JUNE-95
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/762,762
FILING DATE: 16-SEPT-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/01746
FILING DATE: 14-MAR-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/615,784
FILING DATE: 14-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/567,373
FILING DATE: 13-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/494,106
FILING DATE: 16-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Lassen, Elizabeth
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 69-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510

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alignment_block: ..  
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Align seg 1/1   to: US-08-471-791-12    From: 1      to: 1533
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sequence 12, Application PC/TUS9101746
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GENERAL INFORMATION: Thompson, Gregory A  
APPLICANT: Knaut, Vic C  
TITLE OF INVENTION: Plant Desaturases-Compositions and Uses  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS: plant  
ADDRESSEE: Calgene, Inc.  
ADDRESS: 1020 Fifth Street  
STREET: Davis  
CITY: Davis  
STATE: California  
COUNTRY: USA  
ZIP 95616

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COMPUTER READABLE FORM: 3.50 inch, 1.0 MB storage
MEDIUM TYPE: Diskette
COMPUTER: Apple Macintosh 6.0.7
OPERATING SYSTEM: Macintosh 4.0
SOFTWARE: Microsoftword
CURRENT APPLICATION NUMBER: PCT/US91/01746
APPLICATION NUMBER: 19910314
FILING DATE: 19910314
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/615,784
FILING DATE: 14-NOV-1990
APPLICATION NUMBER: 07/567,373
FILING DATE: 13-AUG-1990
FILING DATE: 07/494,106
APPLICATION NUMBER: 16-MAR-1990
FILING DATE: 16-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Lassen, Elizabeth
REGISTRATION NUMBER: 31,845
NAME: Donna E. Schaefer
REGISTRATION NUMBER: 34,719
REFERENCE/DOCKET NUMBER: CGNE 69-3 WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
TELEX: 350370 CGNE 12:
INFORMATION FOR SEO ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1533 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
PCT-US91-01746-12

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alignment_scores:	Length:	149
Quality:	Gaps:	5
Ratio:	Percent Identity:	20.134
Percent Similarity:		44.966

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alignment block:
US-09-722-838-2 x PCT-US91-01746-12 ..
Align seg 1/1 to: PCT-US91-01746-12 from: 1 to: 1533

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66 ysAspserIylsgIysnproIalrpoarGlyralaValIyr..... 618
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79 ..... 668
619 TGGACAGCTGAGAGACAGCAGCATGGCGATCTTCTCCACACCTATCTCA 84
      ::::: ::::: ::::: ::::: :::::
80 .....AspValGluIyrA 84
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669 CCTTTCTGGCGGGTAGACATGACAGGACAGANTACAGACATTTCAGTATTC 718
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seq_documentation_block:
; Sequence 32, Application PC/TUS9105801
; GENERAL INFORMATION:
; APPLICANT: Vic. C. Knauf
; APPLICANT: Gregory A. Thompson
; TITLE OF INVENTION: Plant Fatty Acid Synthases
; NUMBER OF SEQUENCES:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: CA
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.7
; SOFTWARE: Microsoft Word 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/05801
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/568,493
; FILING DATE: 15-AUGUST-1990
; PRIOR APPLICATION DATA: 07/721,761
; APPLICATION NUMBER:
; FILING DATE: 26-JUNE-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth Laasen
; REGISTRATION NUMBER: 31,845
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; REFERENCE/DOCKET NUMBER: CGNE 76-2 WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (916) 753-6313
; TELEFAX: (916) 753-1510
; INFORMATION FOR SEQ. ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1533 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; PCT-US91-05801-32

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; GENERAL INFORMATION:
; APPLICANT: STILLMAN, Bruce
; APPLICANT: BELL, Stephen P
; APPLICANT: KOBAYASHI, Ryuji
; APPLICANT: RINE, Jasper
; APPLICANT: FOSS, Margit
; APPLICANT: McNALLY, Francis J
; APPLICANT: LAURENSEN, Patricia
; APPLICANT: HERSKOWITZ, Ira
; APPLICANT: LI, Joachim J
; APPLICANT: GAVIN, Kimberly
; TITLE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; APPLICATION NUMBER: US/08/484,105
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman Ph. D., Richard Aron
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: A-59032/DJB/RAO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 494-8700
; TELEFAX: (415) 494-8771
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APPLICANT: Masure, Robert
TITLE OF INVENTION: Antibody Recognizing Endothelial Cell
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESS: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,353
FILING DATE: 30-NOV-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Jackson, David
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-097CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3744
PUBLICATION INFORMATION:
AUTHORS: Delisse-Gathoye, et al.
TITLE: Cloning, Partial Sequence, Expressions, and
TITLE: Antigenic Analysis of the Filamentous
JOURNAL: Hemagglutinin Gene of Bordetella Pertussis
VOLUME: 58
ISSUE: 9
PAGES: 2895-2905
DATE: September-1990
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seq_documentation_block:
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Patent No. 5968512
GENERAL INFORMATION:
APPLICANT: Tuomanen, Elaine
APPLICANT: Masure, Robert
TITLE OF INVENTION: Antibody Recognizing Endothelial Cell
TITLE OF INVENTION: Ligand for Leukocyte CR3
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESS: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,965
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/348,353
FILING DATE: 30-NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/247,572
FILING DATE: 23-MAY-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/03725
FILING DATE: 04-MAY-1992
CLASSIFICATION: 424
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Wed Jan 30 11:57:33 2002

us-09-722-838-2.rn1

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Patent No. 5993827
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Chltnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellens, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESS: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CPI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-0176
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 8220 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE: Plasmodium falciparum
ORGANISM: Plasmodium falciparum
US-08-487-826B-11
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Ratio: 1.190 Gaps: 5
Percent Similarity 57.426 Percent Identity: 28.713
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Patent No. 5993827
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Chltnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellens, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESS: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CPI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-0176
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
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Date: Jan 29, 2002 9:30 PM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 Compugen Ltd.

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XX 13-MAR-2001 (first entry)

DE Aspergillus oryzae EST SEQ ID NO:5109.

XX Multiple gene expression: filamentous fungal cell; EST;

KM expressed sequence tag; Fusarium venenatum; Aspergillus niger;

KM Aspergillus oryzae; Trichoderma reesei; Identification; recombination;

KM culture condition; environmental stress; spore morphogenesis;

KM metabolic pathway engineering; catabolic pathway engineering; ss.

OS Aspergillus oryzae.

PN WO200056762-A2.

PD 28-SEP-2000.

PF 22-MAR-2000; 2000WO-US07781.

PR 22-MAR-1999; 9905-0273623.

XX (NOVO) NOVO NORDISK BIOTECH INC.

XX (NOVO) NOVO NORDISK AS.

XX Berta RM, Rey MM, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;

XX WPI: 2000-594572/56.

XX Monitoring differential expression of genes in filamentous fungal cells

XX substrate of expressed sequence tags -

XX Claim 88; Page 2142; 3161pp; English.

XX The present invention describes a method for monitoring differential

XX expression of genes in a first filamentous fungal (FF) cell relative to

XX expression of the same genes in one or more second filamentous fungal

XX cells. The method uses fluorescence-labeled nucleic acids isolated from

XX the FF cells and a substrate of expressed sequence tags (EST). The ESTs

XX are used in the methods for monitoring differential expression of genes

XX in a first filamentous fungal (FF) cell relative to expression of the

XX same genes in one or more second filamentous fungal cells. Monitoring

XX the global expression of genes from FF cells allows the production

XX potential of the microorganisms to be improved. New genes may be

XX discovered, possible functions of unknown open reading frames can be

XX identified and gene copy number variation and stability can be

XX monitored. The expression of genes can be used to study how FF cells

XX adapt to changes in culture conditions, environmental stress, spore

XX morphogenesis, recombination, metabolic or catabolic pathway

XX engineering. Using ESTs provides several advantages over genomic or

XX random cDNA clones including elimination of redundancy as one spot on an

XX array equals one gene or open reading frame, and organisation of the

XX microarrays based on function of the gene products to facilitate

XX analysis of the results. AAF07478 to AAF11247 represents ESTs from

XX Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus

XX niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and

XX AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are

XX all specifically claimed in the present invention.

XX Sequence 801 BP; 222 A; 206 C; 174 G; 199 T; 0 other;

Wed Jan 30 11:57:32 2002

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117 GlnAsnLeuLysAsnAlaLeuAsnIleHisThrSerIleHisAlaAspA 134
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134 sPLysGlyAspIleGluTrpLysThrValLeuAlaGluAlaSerGlyGly 150
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151 LysAlaGlyLys 154
589 AAGCTGTGTAAG 600

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XX 13-MAR-2001 (first entry)
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XX Multiple gene expression: filamentous fungal cell; EST;
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XX Aspergillus oryzae; Trichoderma reesei; identification; recombination;
XX culture condition; environmental stress; spore morphogenesis;
XX metabolic pathway engineering; catabolic pathway engineering; ss.
XX
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XX WO200056762-A2.
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XX 28-SEP-2000

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XX PF 22-MAR-2000; 2000WO-US07781.
XX PR 22-MAR-1999; 99US-0273623.
XX PA (NOVO) NOVO NORDISK BIOTECH INC.
XX PA (NOVO) NOVO NORDISK AS.
XX PI Berka RM, Key MW, Shuster JR, Kaupinen S, Clausen IG, Olsen PB;
XX DR WPI: 2000-594572/56.
XX PT Monitoring differential expression of genes in filamentous fungal cells
XX PT uses fluorescence-labeled nucleic acids isolated from the cells and a
XX PI substrate of expressed sequence tags -
XX PS Claim 86; Page 779-780; 3161pp; English.
XX CC The present invention describes a method for monitoring differential
XX CC expression of genes in a first filamentous fungal (FF) cell relative to
XX CC expression of the same genes in one or more second filamentous fungal
XX CC cells. The method uses fluorescence-labeled nucleic acids (EST). The ESTs
XX CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs
XX CC are used in the methods for monitoring differential expression of the
XX CC in a first filamentous fungal (FF) cell relative to expression of the
XX CC same genes in one or more second filamentous fungal cells. Monitoring
XX CC the global expression of genes from FF cells allows the production
XX CC potential of the microorganisms to be improved. New genes may be
XX CC discovered, possible functions of unknown open reading frames can be
XX CC identified and gene copy number variation and stability can be
XX CC monitored. The expression of genes can be used to study how FF cells
XX CC adapt to changes in culture conditions, environmental stress, spore
XX CC morphogenesis, recombination, metabolic or catabolic pathway,
XX CC random DNA clones including elimination of redundancy as one spot on an
XX CC array equals one gene or open reading frame, and organization of the
XX CC microarrays based on function of the gene products to facilitate
XX CC analysis of the results. AAF07478 to AAF11247 represents ESTs from
XX CC Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus
XX CC niger; AAF11854 to AAF14878 represents ESTs from Trichoderma reesei, which are
XX CC all specifically claimed in the present invention.
XX SQ Sequence 959 BP; 236 A; 266 C; 215 G; 239 T; 3 other:

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272 CTGACGACTACACAGAGATTGTTGCGAAGAGCCTCCGAGAGCGCGCAGC 321
55 TyrGluValPheArgSerArgLeu...GluAlaThrLysAspSerLysG 70
322 TGGGAGGACTTCGCGAGACGCTCGTCAACGCTACCGCCAGAGCGGAGC 371
70 Y.....AsnProAlaProArgTyrAlaValTyrAspValGluTyrA 84

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DT 18-OCT-2000 (first entry)
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DE Zea mays DNA fragment SEQ ID NO: 43960.
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KM Hybridisation assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway; metabolic;
KM pathway; promoter; termination sequence; corn; ss.
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OS Zea mays subsp. mays.
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PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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Percent Similarity: 68.345

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XX Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway;
XX metabolic pathway; promoter; termination sequence; ss.
OS Arabidopsis thaliana.
PN EP1033405-A2.
XX 06-SEP-2000.
PD 25-FEB-2000; 2000EP-0301439.
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 Quality: 177.00 Gaps: 6  
 Ratio: 1.863  
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 US-09-722-838-2 x AAC33228

Align seg 1/1 to: AAC33228 from: 1 to: 786

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AC AAC34886;
XX 17-OCT-2000 (first entry)
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 8245.
XX Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway;
XX metabolic pathway; promoter; termination sequence; ss.
OS Arabidopsis thaliana.
XX EP1033405-A2.
XX 06-SEP-2000.
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Percent Similarity:	67.626	Percent Identity:	30.935

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20 eArgMetSerGlyAlaSpGlyAlaValIleAspGluValSerGlnGlu 36  
:|||||.....  
182 G.....AAGCGAAAGACACACCGCTTCATTCATCTACA 216  
36 ystIleAlaSpAsnLysGlyValIleAspGluValSerGlnGlu 52  
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217 AGATTGAGAGAGAGAGAGAGAGAGATGATGAGAGAGAGAGAGAG 266  
53 ...GluAspTyrGluValPheArgSerArgLeuGluAlaThrLysAspSe 68  
|||||.....  
267 ATTCTACTACGACGAGACTTGCAGCAAGCTTCAGCTGACGAA..... 311  
68 rLysGlyAsnProAlaProArgTyrAlaValIleAspGluValSerGln 85  
312 .....TGCGATACCGCATTTAGATTGACATT.....G 342  
85 euGlyGlyGlyGlyGlyValSerGlySerLysIleValPheIleSerTPVal 101  
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343 TCACTGCGAGAGATTCGACAGAGAGAGAGATTCCTCATTCATGCTGT 392  
102 ProSerAspThrProThrLeuTyrPheSerMetLeuTyrAlaSerThrArg 118  
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393 CCCGACGTACCAAGGTGAGAGAGAGAGAGATGATGAGAGAGAGAGAG 442  
118 uAsnLeuLysAsnAlaLeuAsn...IleHisThrSerIleHisAlaAsp 134  
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XX Hybridisation assay: genetic mapping; gene expression control;  
KM protein identification; signal transduction pathway;  
KM metabolic pathway; promoter; termination sequence; ss.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EPI033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-0301439.  
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  05-JUL-2000 (first entry)

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  XX variety identification; genetic variability evaluation; primer; ss.

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  OS Eucalyptus grandis.

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  XX MO9967421-A1.

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  XX 29-DEC-1999.

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  PD 25-JUN-1999; 99WO-NZ00092.

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  PF 25-JUN-1998; 98US-0105307.

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  XX (GENE-) GENESIS RES & DEV CORP LTD & FLETCHER.

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  PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.

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  XX Havukkala IJ, Bloksberg LN, Glenn M;

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  XX WPI; 2000-116958/10.

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  PT New plant microsatellite markers and associated flanking species for

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  XX the detection of polymorphic genetic markers -

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  PS Claim 1; Page 332-333; 392pp; English.

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  CC Sequences AAA31040-A32093 represent novel plant microsatellite sequences
  CC and associated flanking species. The sequences comprise a central core
  CC repeat sequence, especially selected from the sequences AAA32094-A32096
  CC with left and right flanking sequences. The polynucleotide sequences

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CC can be used in the detection of DNA polymorphisms, in genome mapping,  
CC in physical mapping, in positional cloning of genes, in variety  
CC identification and in evaluation of genetic variability within and  
CC between plant tissues, populations, cultivars, species and species  
CC groups. They may also be used to design hybridization probes for  
CC oligonucleotide fingerprinting and library screening and to design  
CC primers for microsatellite-primed PCR. Microsatellite markers are  
CC useful to locate specific economically useful genes in plant genomes.  
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Ratio: 1.946 Gaps: 5  
Percent Similarity: 67.742 Percent Identity: 31.452  
  
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: |||||.....  
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36 ySileAlaAspAsnLysLysGluValIleAlaAspGluValSerGln... 51  
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52 GluGluAspTyrGluValPheArgSerArgLeuGluAlaThrLysAspSe 68  
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XX  
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XX  
XX Hybridisation assay; genetic mapping; gene expression control;  
KM protein identification; signal transduction pathway;  
KM metabolic pathway; promoter; termination sequence; ss.  
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PN EP1033405-A2.  
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PR 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
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PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
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PR 02-JUL-1999; 99US-0142154.  
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PR 06-JUL-1999; 99US-0142390.
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PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
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PR 27-AUG-1999; 99US-0151065.
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PR 01-SEP-1999; 99US-0151930.
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PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
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PR 23-SEP-1999; 99US-0155486.
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PR 29-SEP-1999; 99US-0156596.
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PR 28-OCT-1999; 99US-0162142.

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alignment\_scores: Quality: 163.00 Length: 138  
Ratio: 1.734 Gaps: 7  
Percent Similarity: 68.116 Percent Identity: 31.884

alignment\_block: US-09-722-838-2 x AAC40094 ..

Align seg 1/1 to: AAC40094 from: 1 to: 659

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|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
126 GCGTCGGGATGCGGCGTGGAGGAGCGAGTGAAGCTGAAGCTTTTGGAGCT 175
20 eargMetSerGlyAsnLysAlaAsnLysThrLysPheIleIlePheLysI 37
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
176 AAAAGCAAGAGAAAC.....TATAGGTCATTAATTTGAGCA 213
37 leAlaspAsnLysLysGluValValIleAspGluVal...SerGluGlu 52
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
214 TA.....GATGCAACAAGAGTGTGTAAGAAAGCTGGGAAAGCCCA 257
53 GluAspTyrGluValPheArgSerArgLeuGluAlaThrLysAspSerLys 69
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
258 GAGACACTACGACGATTACCACTTACCTACCGCCCAATGAA..... 299
69 sGlyAsnProAlaProArgTyrAlaValTyrAspValGluTyrAspLeu 86
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
300 .....TGCCGCTACGCGCGTTTATGAC.....TTGACACTCA 330
86 LysGlyGlyGlyGly...LysArgSerLysIleValPheIleSerTPVal 101
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PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
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PR 12-AUG-1999; 99US-0148341.
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PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151080.
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PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
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PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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alignment\_scores: 162.00  
Quality: 1.670  
Ratio: 1.670

Length: 146  
Gaps: 5

Percent Similarity: 66.438 Percent Identity: 28.082

alignment\_block:  
US-09-722-838-2 x AAC42280 ..

Align seg 1/1 to: AAC42280 from: 1 to: 690

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21 GmetSerGlyAsnLysAlaAsnLysThrLysPheIleIlePheLysIleA 38
: : : : : : : : : : : : : : : : : : : : : : : : :
231 A.....AGCAAAACCTCATCGCTATGCTGTCTTCAAGATTG 268
38 IaAspAsnLysGluValValIleAspGluVal...SerGlnGlu 53
: : : : : : : : : : : : : : : : : : : : : : : : :
269 ATGAATCCAAAAAGAAAGATTGTTGTGAGAAAACGAAATCCACAGAG 318
54 AspTyrGluValPheArgSerArgLeuGluAlaThrLysAspSerLysG 70
: : : : : : : : : : : : : : : : : : : : : : : : :
319 AGCTACGATGATTTCTTACGTTCACTTCTT..... 348
70 YAsnProAlaProArgTyrAlaValTyrAspValGluTyrAspLeuGly 87
: : : : : : : : : : : : : : : : : : : : : : : : :
349 .GATAAATGACTGCAGATACGCTGTTATGACTTGTATTC...GTTACTT 394
87 LYLGLYLGLYLysArgSerLysIleValPheIleSerTyrValProSer 103
: : : : : : : : : : : : : : : : : : : : : : : : :
395 CTGAGAAATTCMAAAGAGCAAAATCTCTTCTTGTGCTGCTTCGCG 444
104 AspThrProThrLeuTyrPheSerMetLeuTyrAlaSerThrArgGluAsn 120
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136 LysAspIleGluTyrPheValLeuAlaGluAlaSer 148
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XX 06-OCT-2000 (first entry)
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DE
XX
XX Human, 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
OS Homo sapiens.
PN EP1033401-A2.
PD 06-SEP-2000.
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XX 21-FEB-2000; 2000EP-0200610.
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XX Dumas Mline Edwards J, Duclert A, Giordano J;
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XX WPI; 2000-500381/45.
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XX P-PSDB; AAG03978.

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PR 27-JUL-1999; 99US-0145913.
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PR 27-JUL-1999; 99US-0145919.
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PR 29-OCT-1999; 99US-0162142.

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Percent Similarity: 67.857   Percent Identity: 29.286

alignment\_block:  
 US-09-722-838-2 x AAC49221 ..

Align seg 1/1 to: AAC49221 from: 1 to: 708

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174 G.....AAGCGAAGAGACACACCGCTTCATCATTTACA 208
36  ysIleAlaSpAsnGlySerGluValIleAlaSpGLuValserGlnGlu 52
   |||||... |||...
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53  ..GluAspTyrGluValPheArgSerArgLeuGluAlaThrLysAspSe 68
259 GGTCAACCATGAGGAGGACCTGCTCCAGTCTCCAGCTGATGAA..... 303
68  rlyGlyAsnProAlaProArgTyrAlaValTyrAspValGluTyrAspL 85
304 .....TGCGCTATGCCATTTCGAT.....TTGATP 331
85  euGlyGlyGlyGlyGly..LysArgSerLysIleValAlaPheIleSerTrp 100
   :|||... |||...
332 TTGTGATGCTCTGAGGATGCCAGAGAGAGATTTTTCGTGACGAGG 381
101 ValProSerAspThrProThrLeuTrpSerMetIleTyrAlaSerThrAr 117
   |||||... |||...
382 TCTCCGACACACAGACAGAGTGAACCAAGATGATCTATGCCAGCTCCA 431
117 gGluAsnLeuLysAsnAlaLeuAsn...IleHisThrSerIleHisAla 133
432 GCACAGCTTCAGAGAGAGACTGACAGCAATTCAGTCAGCTTCAGGCA 481
133 sPAspLysGlyAspIleGlu 139
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XX AAC37069;
XX 17-OCT-2000 (first entry)
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 16066.
XX
XX Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway;
XX metabolic pathway; promoter; termination sequence; ss.
OS Arabidopsis thaliana.
XX

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PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PE 25-FEB-2000; 2000EP-0301439.  
XX  
PR 25-FEB-1999; 99US-0121825.  
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Align seg 1/1 to: AAC37069 from: 1 to: 710

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XX Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway;
XX metabolic pathway; promoter; termination sequence; ss.
OS Arabidopsis thaliana.
XX EP1033405-A2.
XX 06-SEP-2000.
XX 25-FEB-2000; 2000EP-0301439.
XX 25-FEB-1999; 99US-0121825.
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DT 18-OCT-2000 (first entry)

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XX Hybridisation assay; genetic mapping; gene expression control;

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KW pathway; promoter; termination sequence; corn; ss.

XX Zea mays subsp. mays.

XX EP1033405-A2.

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440 GTCCTCCGAACTGCGCAAAAGTGAAGACAGACAGATGATTTTACGCGACTTA 489
117 rrgGluAsnLeuLysAsnAlaLeuAsn...IleHisThrSerIleHisAla 132
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KM protein identification; signal transduction pathway;
XX metabolic pathway; promoter; termination sequence; ss.
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XX
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XX
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US-09-722-838-2 x AAC42775 . .

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23 rGlyAsnTysAlaAsnLysThrLysPheIleIlePheLysIleAlaAspA 40
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106 ProThreutPseMetIleTyAlaSerThrArgLusInLeuLysAs 122
      ::||::|.....|
259 AGCGTAGAGATGAGATGCTGTATGCACAAGCCTCTAACATGATTAAAG 308
      :||::|.....|
122 nAlaLeuasn..IleHisTrpSerIleHisAlaAspAspLysAspi 138
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309 AGAATTGACGCGCATTCAGGTGGAGATTCAACAGCCACATGATCTTAAGCAGA 358
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ID AAA31506 standard;

AC AAA31506;

DT 05-JUL-2000 (first entry)

Plant microsatellite marker #467.

**KW** Plant microsatellite sequence; core repeat sequence; detection; probe;

KW DNA polymorphism; genome mapping; physical mapping; fingerprinting  
 KW variety identification; genetic variability evaluation; primer; ss  
 XX  
 OS *Eucalyptus grandis*.

PN WO9967421-A1

PD 29-DEC-1999.

PF 25-JUN-1999; 99WO-NZ00092

PR 25-JUN-1998; 98US-0105307.

PA (GENE-) GENESIS RES & DEV CORP LTD & FLETCHER

XX

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3  
4  
5  
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7  
8  
9  
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11  
12

XX

PT the detection of polymorphic genetic markers.

PS Claim 1; Page 214; 392pp; English.

CC Sequences AA331040-A32093 represent novel plant microsatellite sequences  
CC and associated flanking species. The sequences comprise a central core  
CC repeat sequence, especially selected from the sequences AA332094-A32096  
CC with left and right flanking sequences. The polynucleotide sequences  
CC can be used in the detection of DNA polymorphisms, in genome mapping,  
CC in physical mapping, in positional cloning of genes, in variety  
CC identification and in evaluation of genetic variability within and  
CC between plant tissues, populations, cultivars, species and species  
CC groups. They may also be used to design hybridization probes for  
CC oligonucleotide fingerprinting and library screening and to design  
CC primers for microsatellite-primed PCR. Microsatellite markers are  
CC useful to locate specific economically useful genes in plant genomes.  
XX  
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US-09-722-838-2 x AAA31506

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36 ysilealaspasnlyslgluvalvalileaspgluvalsergin... 51

210 AGATTGAAGAGAGCAAAAGCAAGTGATCGTTGAAAAACTTGGAGAACCT .25

52 GLUGLUASPTYRGluValPheArgSerArgLeuGLuAlaThrLysaspSe 68

260 GCAATAGTTATGAGATTCTACTGCAAGCCTTCCTGCTGATGAG... 30

68 RLYSGLYASNPROALAProARGTYRAlaValTYRASPValGLUTYRASPL 85

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 VERSION AL112286.1 GI:5826905  
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 SOURCE Botryotinia fuckeliana.  
 ORGANISM Botryotinia fuckeliana  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;  
 Helotiales; Sclerotiniaceae; Botryotinia.  
 REFERENCE 1 (bases 1 to 720)  
 AUTHORS Bilton,F., Lewis,C., Fortini,D., Pradier,J.M. and Brygoo,Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr,

78026 Versailles, France  
 2 (bases 1 to 720)  
 Genoscope.  
 DIRECT Submission  
 JOURNAL Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage :  
 CP 5706 91057 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr  
 - Web : www.genoscope.cns.fr)  
 The cDNA library to be analyzed within the framework of this  
 project was created using a Botrytis cinerea strain which was grown  
 under conditions of nitrogen deprivation, which is the normal  
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 US-09-722-838-2 x CNS0192A ..

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445 TCCTCGATGATGCAGATACCTTCCCTAAATGATGATGAGCTCCACCAA 494
117  gGIuAsnLeuLYsAsnAlaLeuAsn.....IleHisThrSerIleHisA 132
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
495 GGAATCTTCAAGCGTGTATTCGGACTTTCGGCGCATGAACTCCCAAG 544
132  laAspAspLYsGLyAspIleArgIuTrpLYsThrValLeuAlaGLuLase 148
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
545 CAACAGATGAAGCCGACCTCGAAGAGATGATGTGAAGACACTCAGC 594
149  gLYsLYsAla 152
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595 AAGGTACAGCC 606

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seq_name: gb_pl:CNS019LK
seq_documentation_block:
LOCUS      CNS019LK      696 bp      mRNA      PLN      02-SEP-1999
DEFINITION Botrytis cinerea strain T4 cDNA library under conditions of
             nitrogen deprivation.
ACCESSION   AL111792.1 GI:5826411
VERSION     AL111792.1
KEYWORDS    CDNA library; nitrogen deprivation.
SOURCE      Botryotinia fuckeliana.
ORGANISM    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
             Helotiales; Sclerotiniaceae; Botryotinia.
REFERENCE   1 (bases 1 to 696)
AUTHORS     Bitton,F., Lewis,C., Fortini,D., Pradier,J.M. and Brygoo,Y.
TITLE       Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr,
JOURNAL     78026 Versailles, France
REFERENCE   2 (bases 1 to 696)
AUTHORS     Genoscope.
TITLE       Direct Submission
JOURNAL     Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage :
             CP 5706 91057 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
COMMENT     - Web : www.genoscope.cns.fr)
             The cDNA library to be analyzed within the framework of this
             project was created using a Botrytis cinerea strain which was grown
             under conditions of nitrogen deprivation, which is the normal
             situation for B. cinerea during its development on its host plant.
             The library was produced in an oriented direction, in the pBSIT
             vector.
FEATURES
    source          1..696
                     /organism="Botryotinia fuckeliana"
                     /strain="T4"
                     /db_xref="taxon:40559"
                     /note="Genoscope sequence ID : W67H111"
BASE COUNT      211 a      171 c      150 g      161 t      3 others
ORIGIN
alignment_scores:
    Quality: 290.00      Length: 154
    Ratio: 2.566      Gaps: 3
    Percent Similarity: 73.377      Percent Identity: 40.260
alignment_block:
US-09-722-838-2 x CNS019LK ..
Align seg 1/1 to: CNS019LK from: 1 to: 696
5  SerGlyValSerIleAlaSpGluCysIleThrAlaPheAsnAspPheAr 21
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
162 TCAGATGATCACCGTCGACGAGAAATGCATGCATCAACGAGATGAA 211
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
21  gmetSerGlyAsnLysAlaAsnLysThrLysPheIleIlePheLysIleA 38
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
212 GCTTCAA.....AAGAGATCAAGTGATTGTTTACAAGATCA 249
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
38  laaspaSnLysLysGluValValIleAspGluValSerGlnGluAsp 54
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
250 ACGATGAAGCACAAGGTCGTCGACACTCCAGCGAGTCGGCAGAC 299
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
55  TyrGluValPheArgSerArgLeu.....GluAlaThrLysAs 67
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
300 TGGGAACCATTCCTCGTAGCTCTGTAAGCAAGCAAGCACTCAACAA 349
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67  pSerLysGlyAsnProAlaProArgTyrAlaValTyrAspValGluTyr 84
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
350 CAATACCCAGGTAAGGTCGCGATATGCTGTATGACTTCACACTACG 399
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
84  splenGlyLysGlyLysGlyLysArgSerLysIleValPheIleSerTP 100
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
400 ATTTGCCAAGCAGAGAGGACAAGAACCAAGCTTACTTCACTTTCGTG 449

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101 ValProSerAspThrProThrLeuTrpSerMetIleTyrAlaSerThrAr 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
450 TCCCTTGATGATGCCAGTACCTTCCTTAATAATGATGATGCGCTCACCA 499
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
117  gLuAsnLeuLysAsnAlaLeuAsn.....IleHisThrSerIleHisA 132
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
500 GGAATCTTTCAGAGCGTCTTATCCGACCTTCGGGGGAGATCACTCCAG 549
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
132  laaspaSpLysGlyAspIleGluTrpLysThrValIleAlaGluAlaSer 148
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
550 CAAAGATGAAGCCGACCTCGAAGAGATGAGATGTAAGACACTCAGC 599
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
149  GlyLysLysAla 152
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
600 AAGCGTACAGCC 611
seq_name: gb_pl:CNS01DF7
seq_documentation_block:
LOCUS      CNS01DF7      576 bp      mRNA      PLN      03-SEP-1999
DEFINITION Botrytis cinerea strain T4 cDNA library under conditions of
             nitrogen deprivation.
ACCESSION   AL116747
VERSION     AL116747.1 GI:5831963
KEYWORDS    CDNA library; nitrogen deprivation.
SOURCE      Botryotinia fuckeliana.
ORGANISM    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
             Helotiales; Sclerotiniaceae; Botryotinia.
REFERENCE   1 (bases 1 to 576)
AUTHORS     Bitton,F., Lewis,C., Fortini,D., Pradier,J.M. and Brygoo,Y.
TITLE       Direct Submission
JOURNAL     Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr,
             78026 Versailles, France
REFERENCE   2 (bases 1 to 576)
AUTHORS     Genoscope.
TITLE       Direct Submission
JOURNAL     Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage :
             CP 5706 91057 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
COMMENT     - Web : www.genoscope.cns.fr)
             The cDNA library to be analyzed within the framework of this
             project was created using a Botrytis cinerea strain which was grown
             under conditions of nitrogen deprivation, which is the normal
             situation for B. cinerea during its development on its host plant.
             The library was produced in an oriented direction, in the pBSIT
             vector.
FEATURES
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                     /strain="T4"
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                     /note="Genoscope sequence ID : W56A091"
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    Ratio: 2.541      Gaps: 3
    Percent Similarity: 73.649      Percent Identity: 40.541
alignment_block:
US-09-722-838-2 x CNS01DF7 ..
Align seg 1/1 to: CNS01DF7 from: 1 to: 576
11  AspGluCysIleThrAlaPheAsnAspPheArgMetSerGlyAsnLysAl 27
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
4  GAAGATGCATCGAGAACTTCAACGAGATGAAGCTTCA..... 42
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
27  asnLysThrLysPheIleIlePheLysIleAlaAspAsnLysLysGluV 44
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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CDS

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 /note="Essential gene. Part of cortical actin cytoskeleton, and also located in cytoplasm."  
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BASE COUNT 368 a 229 c 209 g 358 t

ORIGIN

alignment\_scores:  
 Quality: 276.00 Length: 149  
 Ratio: 2.579 Gaps: 4  
 Percent Similarity: 71.812 Percent Identity: 38.255

alignment\_block:  
 US-09-722-838-2 x SCCOF1 ..

Align seg 1/1 to: SCCOF1 from: 1 to: 1184

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7 ValSerIleAlaAspGluCysIleThrAlaPheAsnAspPheArgMetSe 23
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
532 GTTGGCTGTCGATGATGATCCCTTACCGCTTTCATGATGATGAAATG.. 579
  23 rglYasnLysAlaAsnLysThrLysPheIleIlePheLysIleAlaAspA 40
  :::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
580 .....GCTAATAAATACAAATTTATTTATTCGATTGCAACGATG 619
  40 snLysLysGluValIleAlaSerGlnGluAlaSerGlnGluAlaSerGlu 56
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
620 CTAAACCGAATGCTGTCTCAAGAAACCTTACTGACCCATCTTACGAT 669
  57 ValPheArgSerArgLeuGluAlaThrLysAspSerLysGlyAsnProAl 73
  :::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
670 GCCTTCTTGAAGAAATTG..... 687
  73 aProArg.....TyrAlaValTyrAspValGluTyrAspLeuG 86
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
688 ..CCAGAAACGACGCTGCTTACGCCATTACGATTTGCAATACGAAATTA 736
  86 lylGlyGlyGluGlyLysArgSerLysIleValIlePheIleSerTrpValPro 102
  :::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
737 ATGCTAATGAGGTAAAGATCCAAAGATTGTTCTTCTCAGCTGTCACA 786
  103 SerAspThrProThrLeuTrpSerMetIleTyrAlaSerThrArgGluAs 119
  :::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
787 GACACTGCTCCAGTCAGATCTAAGATGCTATGCAATCTCCCAAGATGC 836
  119 nLeuLysAsnAlaLeuAsn...IleHisThrSerIleHisAlaAspSpl 135
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
837 CTTAAGAGAGCCCTTAACGCTGTCTACCGATGTTCAAGGACTGATTT 886
  135 ysgLysAspIleGluTrpLysThrValLeuAlaGluAlaSerGlyGly 150

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887 TTTCACCAAGTTCTTACGATCTGTTTGGAAAGAGTCAGACAGAGGC 933

seq\_name: gb\_pl:SCYL050C

seq\_documentation\_block:  
 LOCUS SCYL050C 1194 bp DNA PLN 11-AUG-1997  
 DEFINITION S.cerevisiae chromosome XII reading frame ORF YLL050C.  
 ACCESSION Z73155 Y13138  
 VERSION Z73155.1 GI:1360250  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 baker's yeast.  
 Saccharomyces cerevisiae  
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 1 (bases 1 to 1194)  
 Medler,H., Medler,E., Scharfe,M. and Mambutt,R.  
 Unpublished  
 2 (bases 1 to 1194)  
 MIPS.  
 Direct Submission  
 Submitted (22-MAY-1996) Data collected by MIPS on behalf of the  
 European yeast chromosome XII sequencing project. MIPS at the  
 Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a D-82152  
 Martinsried, FRG; E-mail: Mewes@mips.emblnet.org.  
 Location/Qualifiers  
 1..1194  
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BASE COUNT 363 a 211 c 220 g 400 t

ORIGIN

alignment\_scores:  
 Quality: 276.00 Length: 149  
 Ratio: 2.579 Gaps: 4  
 Percent Similarity: 71.812 Percent Identity: 38.255

alignment\_block:  
 US-09-722-838-2 x SCYL050C/rev ..

Align seg 1/1 to reverse of: SCYL050C from: 1 to: 1194

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7 ValSerIleAlaAspGluCysIleThrAlaPheAsnAspPheArgMetSe 23
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
749 GTTGGCTGTCGATGATGATCCCTTACCGCTTTCATGATGATGAAATG.. 702
  23 rglYasnLysAlaAsnLysThrLysPheIleIlePheLysIleAlaAspA 40
  :::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
701 .....GCTAATAAATACAAATTTATTTATTCGATTGCAAGCAGT 662
  40 snLysLysGluValIleAlaSerGlnGluAlaSerGlnGluAlaSerGlu 56

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661 CTTAAACCGAATCGTTGCAAGAAACCTACGACCATCTTACGAT 612
57 ValPheArySerArgLeuGluAlaThrIlyAspSerIlyGlyAsnProAl 73
611 GCCTTCTTAGAGAAATG..... 594
73 aProArg.....TyrAlaValTyrAspValGluTyrAspLeuG 86
593 .CCAGAAACGACGCTCTTTACGCCATTACGATTTTGAAATCGAAATTA 545
86 IlyGlyGlyGluGlyAspSerIlyValAlaPheIleSerTyrValPro 102
544 ATGTAATGAAGTAAGATCAAGATGTTTCTTCACTGAGCTCCA 495
103 SerAspThrProThrLeuTyrSerMetIleTyrAlaSerThrArgGluAs 119
494 GACACTGCTCCAGTCAGATCGTAAGATGGTCATGCATCTCCACAGAGATGC 445
119 nLeuIlyAsnAlaLeuAsn...IleHisThrSerIleHisAlaAspAl 135
444 CTTAAGAAAGCCTTAAACGGGTGCTCTACCGATGTTCAAGTACTGATT 395
135 ySgIlyAspIleGluTyrIlyThrValLeuAlaGluAlaSerGlyIly 150
394 TTTCGGAAGTTTCTTACGATCTGTTTGAAAGAGTCAGACGAGGC 348

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seq\_name: gb\_pl:YSCCOF

seq\_documentation\_block:

LOCUS YSCCOF 2005 bp DNA PLN 01-FEB-2000  
DEFINITION Saccharomyces cerevisiae COF1 gene for cofilin, complete cds.

ACCESSION D13230.1 GI:287599

KEYWORDS cofilin.

SOURCE Saccharomyces cerevisiae (strain:X21801A) DNA.

ORGANISM Saccharomyces cerevisiae

REFERENCE Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
1 (sites)

AUTHORS Iida,K., Moriyama,K., Matsumoto,S., Kawasaki,H., Nishida,E. and  
Yahara,I.

TITLE Isolation of a yeast essential gene, COF1, that encodes a homologue  
of mammalian cofilin, a low-M(r) actin-binding and depolymerizing  
protein

JOURNAL Gene 124 (1), 115-120 (1993)

MEDLINE 93178959

REFERENCE 2 (bases 1 to 2005)

AUTHORS Iida,K.

JOURNAL unpublished (1993)

COMMENT Submitted (16-SEP-1992) to DDBJ by:  
Kazuko Iida

The Tokyo Metropolitan Institute of  
Medical Science

3-18-22 Honkomagome, Bunkyo-ku  
Tokyo 113

Japan  
Phone: 03-3823-2101 x5202

Email: iida@rinsoken.or.jp

Fax: 03-5685-2932.

Location/Qualifiers

1..2005

FEATURES

source

organism="Saccharomyces cerevisiae"

strain="X21801A"

db\_xref="taxon:4932"

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exon

cds

join(338..351,531..948)

codon\_start=1

product="cofilin"

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BASE COUNT 623 a 395 c 366 g 621 t
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alignment\_scores:  
Quality: 276.00 Length: 149  
Ratio: 2.579 Gaps: 4  
Percent Similarity: 71.812 Percent Identity: 38.255

alignment\_block:  
US-09-722-838-2 x YSCCOF ..

Align seg 1/1 to: YSCCOF from: 1 to: 2005

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7 ValSerIleAlaSpGluCysIleThrAlaPheAsnAspPheArgMetSe 23
532 GTTGCTGTGCTGATGATCCCTTACCGCTTCAATGACTGAAATG.. 579

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23 rGlyAsnIlyAsnIlyThrIlyPheIleIlePheIlyIleAlaAspA 40
580 .....GTAATAATACAAATTTATTTATTCGATGACAGCANG 619

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40 nLysIlyGluValIleAspGluValSerGlnGluIlyAspTyrGlu 56
620 CTTAAACCGAATCGTGTGCAAGAAACCTACGACCATCTTACGAT 669

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57 ValPheArgSerArgLeuGluAlaThrIlyAspSerIlyAsnProAl 73
670 GCCTTCTTAGAGAAATG..... 687

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```

73 aProArg.....TyrAlaValTyrAspValGluTyrAspLeuG 86
688 .CCAGAAACGACGCTCTTTACGCCATTACGATTTTGAAATCGAAATTA 736

```

```

86 IlyGlyGlyGluGlyAspSerIlyValAlaPheIleSerTyrValPro 102
737 ATGTAATGAAGTAAGATCAAGATGTTTCTTCACTGAGCTCCA 786

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103 SerAspThrProThrLeuTyrSerMetIleTyrAlaSerThrArgGluAs 119
787 GACACTGCTCCAGTCAGATCGTAAGATGGTCATGCATCTCCACAGAGATGC 836

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119 nLeuIlyAsnAlaLeuAsn...IleHisThrSerIleHisAlaAspAl 135
837 CTTAAGAAAGCCTTAAACGGGTGCTCTACCGATGTTCAAGTACTGATT 886

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135 ySgIlyAspIleGluTyrIlyThrValLeuAlaGluAlaSerGlyIly 150
887 TTTCGGAAGTTTCTTACGATCTGTTTGAAAGAGTCAGACGAGGC 933

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seq\_name: gb\_pl:SCCH13LST

seq\_documentation\_block:

LOCUS SCCH13LST 37396 bp DNA PLN 26-JAN-1995  
DEFINITION S.cerevisiae chromosome XII DNA including subtelomeric region,of  
left arm.

ACCESSION 247973.1 GI:642313

VERSION 247973.1

KEYWORDS ARS; autonomously replicating sequence; subtelomeric DNA.

SOURCE baker's yeast.

ORGANISM Saccharomyces cerevisiae

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

REFERENCE 1 (bases 1 to 37396)  
AUTHORS Wedler, H. and Wambutt, R.  
TITLE Sequence of a 37 kb DNA fragment from chromosome XII of  
Saccharomyces cerevisiae including the subtelomeric region of the  
left arm  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 37396)  
AUTHORS Wambutt, R.  
TITLE Direct Submission  
JOURNAL Submitted (24-JAN-1995) Rolf Wambutt, AGON Gesellschaft fuer  
molekularbiologische, Technologie mbH, Glienicke Weg 185, Berlin,  
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DOKISRYVRKRPREPSTNDILVAGOKLFGSFEPRDLHOLRCHETIYMDPESVAYQ  
APPGKTEFLHPLIALASKGVYVSEFLPPTVILLANCMITLGRGCLNAPVAPN  
FIEEGCDVLDVYGIYDILASTNPTRIAMENIVECTIRTNVAKLYLIVEFHF  
ETEVYROSQGTINLNDPAFEKALFISGTAPEVADAALQRIGLTILAKSMQINEL  
KRSDELSGLSSTPFRMNLIKESSEVPLGVHVKIMKVSOPREALKLLALFEIEP  
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US-09-722-838-2 x SCCH13LST/rev ..

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23 rGlyasnLyalaasnlYsrThrlYsbHeilellePhelyllleAlaaspa 40
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40 snLyalsglValvalilleaspGlualSerclngluLuaspryrgiu 56
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57 ValPheArgSerArgLeugluAlarThrlysAspserlygLyAsnProal 73
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36904 CTTAGAGAGAGCCTTAACCGTGTCTCTACCCGATGTTCAAGGACTGAT 36855
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seq_documentation_block:
LOCUS CNS01AJK 600 bp mRNA PLN 02-SEP-1999
DEFINITION Botrytis cinerea strain T4 cDNA library under conditions of
nitrogen deprivation.
ACCESSION AL113016
VERSION AL113016.1 GI:5827635
KEYWORDS cDNA library; nitrogen deprivation.
SOURCE Botryotinia fuckelliana.
ORGANISM Botryotinia fuckelliana
Eukaryota; Fungi; Ascomycota; Perizomycotina; Leotiomycetes;
Helotiales; Sclerotiniaceae; Botryotinia.
REFERENCE
AUTHORS 1 (bases 1 to 600)
TITLE Bilton,F., Lewis,C., Fortin,D., Pradler,J.M. and Brygoo,Y.
JOURNAL Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr,
78026 Versailles, France
2 (bases 1 to 600)
Genoscope.
Direct Submission
Submitted (01-SEP-1999) Genoscope - Centre National de Sequençage :
CP 5706 91057 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
COMMENT The cDNA library to be analyzed within the framework of this
project was created using a Botrytis cinerea strain which was grown
under conditions of nitrogen deprivation, which is the normal
situation for B. cinerea during its development on its host plant.
The library was produced in an oriented direction, in the pBSII
vector.
FEATURES
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2 GAATGATGATCGAAGTTCAACGAGATGAGACCTTCAA.....AA 39

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60 ATTTG.....
38 lAspAsnLysLysGLuValValIleAspGLuValSerIngInGLuAsp 54
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71 nProAlProArG.....TYRAlaValTYRAspValGLuTYRAr 84
|||||.....:|.....:|.....:|.....:|
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84 sPLeuGLyGLyGLuGLuLysArGSerLysIleValPheIleSerTP 100
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101 ValProSerAspThrProThrLeuTPSerMetIleTYRAlaSerThrAr 117
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117 gLcLysnLeuLysAsnAlaLeu...AsnIleHsThrSerIleHsAla 133
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133 sPAspLysGLyAspIleGLuTPRlyshThrValLeuAlaGLuAsEr 148
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DEFINITION Pichia angusta cofilin (COF1) mRNA, complete cds.
VERSION AF399639
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ORGANISM Pichia angusta.
Pichia angusta
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Pichia.
1 (bases 1 to 481)
Agaphonov M.O., Deev A.V., Kim S.-Y., Sohn J.-H., Choi E.-S. and
Ter-Avanesyan M.D.
Novel Reporter and Strategy for the Isolation and Functional
Characterization of Transcriptionally Active Sequences in the
Methylotrophic Yeast Hansenula polymorpha
Unpublished
2 (bases 1 to 481)
Agaphonov M.O., Deev A.V., Kim S.-Y., Sohn J.-H., Choi E.-S. and
Ter-Avanesyan M.D.
Direct Submission
Submitted (12-JUL-2001) Institute of Experimental Cardiology,
Cardiology Research Center, 3rd Cherepkovskaya Str. 15A, Moscow

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121552, Russia  
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 DEFINITION Schizosaccharomyces pombe mRNA for actin depolymerizing factor,

complete cds.  
 D89939  
 VERSION D89939.1 GI:1752832  
 KEYWORDS act1; actin depolymerizing factor; cofilin.  
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 ORGANISM Schizosaccharomyces pombe  
 Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 Schizosaccharomycetaceae; Schizosaccharomycetaceae;  
 Schizosaccharomyces.  
 1 (bases 1 to 629)  
 AUTHORS Kawamukai,M.  
 TITLE Direct Submission  
 JOURNAL Submitted (18-DEC-1996) to the DDBJ/EMBL/Genbank databases. Makoto  
 Kawamukai, Shimane University, Life and Environmental Science,  
 Nishikawatsu 1060, Matsue, Shimane 690, Japan  
 (E-mail:kawamukai@life.shimane-u.ac.jp, Tel:0852-32-6587,  
 Fax:0852-32-6587)  
 2 (bases 1 to 629)  
 REFERENCE 2 (bases 1 to 629)  
 AUTHORS Kawamukai,M.  
 TITLE S. pombe cDNA for actin depolymerizing factor  
 JOURNAL Unpublished (1996)  
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293 GCTCCCATTAATCTAAGATGCTTACTCTTCTTAAGATCTTACG 342
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343 TCGGGCTTTACTGGAACTCGTACTGATCAATCAAGCAACGATTTCGCG 392
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LOCUS CNS01918 540 bp mRNA PLN 02-SEP-1999
DEFINITION Botrytis cinerea strain T4 cDNA library under conditions of
nitrogen deprivation.
ACCESSION AL111672.1 GI:5826291
VERSION AL111672.1
KEYWORDS cDNA library; nitrogen deprivation.
SOURCE Botryotinia fuckeliana.
ORGANISM Botryotinia fuckeliana.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Helotiales; Sclerotiniaceae; Botryotinia.
REFERENCE
1 (bases 1 to 540)
Bitton,F., Levis,C., Fortini,D., Pradier,J.M. and Brygoo,Y.
AUTHORS Direct Submission
JOURNAL Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr,
78026 Versailles, France
2 (bases 1 to 540)
Genoscope.
REFERENCE
Direct Submission
Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage :
CP 5706 91057 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT
The cDNA library to be analyzed within the framework of this
project was created using a Botrytis cinerea strain which was grown
under conditions of nitrogen deprivation, which is the normal
situation for B. cinerea during its development on its host plant.
The library was produced in an oriented direction, in the pBSII
vector.
FEATURES
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/note="Genoscope sequence ID : W64H091"
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Percent Similarity: 74.803 Percent Identity: 41.732
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US-09-722-838-2 x CNS01918 ..
Align seg 1/1 to: CNS01918 from: 1 to: 540
32 PheIleIlePheLysIleAlaAspAsnLysGluValValIleAspG 48
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
2 TGATGCTTTTACAAGATCAACAGATGAAGCACAAAGTCGTGTCGACAC 51
48 uValSerGlnGlnGluAspTyrGluValPheArgSerArgLeu..... 62
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
52 TTCGACGAGCTCGCAGACTGCGAACCATTCCGTGAGTCCTCGTAAAG 101

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63 ....GluAlaThrLysAspSerLysGlyAsnProAlaProArgTyrAla 77
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
102 CAAGGCGACTCAACAGAACAAACCCAGGCTAAAGAGGCCAGATATGCT 151
78 ValTyrAspValAlaGluTyrAspLeuGlyGlyGlyGluGlyArgSerLys 94
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
152 GCTCTATGACTTCAACTACAGATTTGGCCAAAGGAGGACAAAGAACCA 201
94 sIleValPheIleSerTyrValProSerAspThrProthleutPserM 111
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
202 GCTTACTTTCATTTGCTGTCCTCGATGATGCCAGTACCTTCCTTAAGA 251
111 eTleTYrAlaSerThrArgGluAsnLysAsnAlaLeuAsn..... 125
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
252 TGATGTACGCTCCACACAGCAAGATCTTCAAGCGTCTTATCCGACTT 301
126 IleHstHrSerIleHsAlaAspAspLysGlyAspIleGtTPrLysTh 142
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
302 TCGGGCGATGAAGTCCAGCAAGATGACCGACCTCGAAGAAATGA 351
142 rValLeuAlaGluAlaSerGlyGlyLysAla 152
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
352 GATGTTGAAGACAGTCAACAGGCTACAGCC 382
seq_name: gb_in:ACAACTPH
seq_documentation_block:
LOCUS ACAACTPH 671 bp mRNA INV 05-OCT-1993
DEFINITION Acanthamoeba castellanii actophorin mRNA, complete cds.
ACCESSION M93361
VERSION M93361.1 GI:155620
KEYWORDS actophorin.
SOURCE Acanthamoeba castellanii cDNA to mRNA.
ORGANISM Acanthamoeba castellanii
Eukaryota; Acanthamoebidae; Acanthamoeba.
REFERENCE
1 (bases 1 to 671)
Quirk,S., MacIver,S.K., Ampe,C., Dobereiner,S.K., Kaiser,D.A.,
Vanhamme,J., Vandekerckhove,J.S. and Pollard,T.D.
AUTHORS Primary structure of and studies on Acanthamoeba actophorin
JOURNAL Biochemistry 32 (33), 8525-8533 (1993)
MEDLINE 93363583
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source location/Qualifiers
1..671
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32..448
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BASE COUNT 173 a 213 c 144 g 141 t
ORIGIN
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Quality: 201.50 Length: 145
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US-09-722-838-2 x ACAACTPH ..
Align seg 1/1 to: ACAACTPH from: 1 to: 671
5 SerGlyValSerIleAlaAspGluCysIleThrAlaPheAsnAspPheAr 21
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
35 TCGGCAATGCTGCTCTGACGATTCGCTCCAGAAATTCAACAGACTCAA 84

```





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EKKEELAFELRLQALKASVKSNNANBNSSSSKNEEVSATMENLISOLQGLCDLSLNMKT
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    complement(6086..8200)
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    cuniculus (Rabbit), KET2-RAB17, Heme-regulated eukaryotic
    initiation factor EIf-2-alpha kinase.", (626aa), fasta
    scores: opt: 438, E:1.2e-19, (30.6% identity in 504 aa)"
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    /product="probable protein kinase"
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    YPSSVQILFQEDSVADLTPTCYSTKNSQIDLEFKEDQADAEHSDCSSTYSQVDT
    LGKIAPTKASSEMILMDSFLEREDECSNIPFDDQPLCLYOMALCEETKEHNR
    RNKHIGVMSKGLRNCYILLFARILEGLYLIDHAMLVHRDLKPRMIFLSSGVHSNR
    SVCLPNSPEDNVEVSNAYEPVNORTLQVPRKIDGGLVLSQSDNIEETSABESF
    VGSTYAPAEIPKSHMRSVMNNSSSTDIYALGILFPELLYPTNTRKRSATLANKG
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    /gene="SPAC20G4.03c"
    /note="PS00108 Serine/Threonine protein kinases
    active-site signature"
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    /gene="SPAC20G4.03c"
    /note="PS00107 Protein kinases ATP-binding region
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    /db_xref="SWISS-PROT:P78955"
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    NQPLTSLTWSGAFSGNIVYHNIPVRLSOSVSVKEPTAPEDCHIFLPQNLFL
    RHVDKYSLSDRITMSANMSEGLQLSVINSARSTKWKGLENELPDSVEDISRH
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    VLTIVISTYVD"
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    /note="ctaccatttaccatcag, splice branch and acceptor
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    /note="gtatgt, splice donor sequence"

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misc_feature      complement(10074..10094)
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                  se quence"
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alignment_block:
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Align seg 1/1 to reverse of: SPAC20G4 from: 1 to: 18437

5 SerGlyValSerIleAlaAspGluCysIleThrAlaPheAsnAspPheAr 21
|||||.....:|||||:|||||.....:
13844 TCAGGTGCAAGAGCTCTCCCGAATGCTTGGAACCTTCCCAAGGCTCAA 13795

21 gMeSerGlyAsnAlaAsnLysThrLysPheIleIlePheLysIleA 38
|||||.....:|||||:|||||.....:
13794 GCTT.....:GGAAGTCACGCCGTTACGTGATTTCAAAATGA 13757

38 laAspAsnLys.....:|||||:|||||.....:
13756 ACGATACCAAGAGTAAGTGAAGAAACGATTAGATGAAATTGAGAAG 13707

41 .....:|||||:|||||.....:
13706 TCCAATATCCCTTTTAAAAATAATTATTTATCTACATGTATATAT 13657

41 .....:|||||:|||||.....:
13656 ATTTATGTTTGAATGCTCTTCATGTCGTTTTTATATATATGTAAC 13607

42 .....:|||||:|||||.....:
13606 CTTTCACTAATTTTTTTTTTGTGTTAGCTGAATAATGTTGAAAAAGAG 13557

50 rGlnGluGluAspTyrGluValPheArgSerArgLysGluAlaIleThrLysA 67
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
13556 TAGGATTAAGACTTCGATATCTTCTGTTGACTTG..CTGAAAAGG 13510

67 sPerLysGlyAsnProAlaProArgTyrAlaValTyrAspValGluTyr 83
|||||.....:|||||:|||||.....:
13509 ATATGC.....CGTATGCTATGATGATTTTGAATTC 13478

84 AspLeuGluGlyGluGluGluValArgSerLysIleValAlaPheIleSerT 100
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
13477 AATCTC.....GGAGAAGGTGTTGTAACAAATATATCTTTATGACTG 13434

100 pAlaProSerAspThrProThrLeuThrPseMetIleTyrAlaSerThra 117
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
13433 GTCTCTGATGTTGCTCCATTAATCAATGAAGTGTTTACTCTTCTTCTTA 13384

117 rGluAsnLeuLysAsnAlaLeu...AsnIleHisThrSerIleHisAla 132
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
13383 AAGATACCTTACCTCGCGCTTTTACGAAATCGTACTGACATCCAAAGA 13334

133 AspAspLysGlyAspIleGluTyrLysThrValLeuAlaGluAlaSer 148

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seq_name: gb_ov:CHKCOF

seq_documentation_block:
LOCUS       CHKCOF               1369 bp      mRNA           VRT          06-MAR-1995
DEFINITION   Chicken cofilin mRNA, complete cds.
ACCESSION    M55659.102915
VERSION      M55659.1 GI:211569
KEYWORDS     cofilin.
SOURCE       Chicken 10-day-old embryo skeletal muscle, cDNA to mRNA, clones
            PCMC-(1,16).
ORGANISM     Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauilia; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE    1 (bases 1 to 1369)
AUTHORS      Abe,H., Endo,T., Yamamoto,K. and Obinata,T.
TITLE        Sequence of cDNAs encoding actin depolymerizing factor and cofilin
            of embryonic chicken skeletal muscle: two functionally distinct
            actin-regulatory proteins exhibit high structural homology
JOURNAL      Biochemistry 29 (32), 7420-7425 (1990)
MEDLINE      91027755
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                LEGGPL"
BASE COUNT   413 a      284 c      291 g      381 t
ORIGIN
alignment_scores:
              Quality: 194.50      Length: 165
              Ratio: 1.835         Gaps: 6
              Percent Similarity: 64.242      Percent Identity: 29.697

alignment_block:
US-09-722-838-2 x CHKCOF ..

Align seg 1/1 to: CHKCOF from: 1 to: 1369

2 AlaleualaSerGlyValSerIleAlaaspGlucylSerThrAlaPheas 18
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
39 GCCATGGCTTCGTGAGTACAGTGAATGATGAAGCATTAAGAAGTTTAA 88
18 naspPhearGmetSerGlyAsnLysAla.....AsnLysT 30
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
89 TGACACTGAAGTAAGAAAATCTTCAACCACAGAGAGATATAAAAAAGAA 138
30 hLySPheHLeIlePhelYsLIeAlaASPsnLYSGluValIle 46
||| :|||||:|||||:|||||:|||||:|||||:|||||:
139 AGAAAGCCCTCTCTTGCTTAAGAGATGACAAAAGCAAATAATCGTA 188
47 AspGluValSerGln.....GluG1 53
:::|||||:|||||:|||||:|||||:|||||:|||||:
189 GAGGAGGGCGACAAGATACGTGCGGTGCATCCGAGATACCGTGGAGGA 238
53 uAspTyrgLuValPheaArgSerArgLeuGluAlaThrIlyAspSerLysG 70

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[illegible]

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/organism="Mus musculus"
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/db_xref="taxon:10090"
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/tissue_type="brain"
/note="24 bp upstream of BamHI site."

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Homo sapiens

KEYWORDS	COLLID.
SOURCE	Human placenta, cDNA to mRNA
ORGANISM	Homo sapiens

## ORGANISM

REFERENCE 1 (bases 1 to 501)  
 AUTHORS Ogawa, K., Tashima, M., Yumoto, Y., Okuda, T., Sawada, H., Okuma, M. and Maruyama, Y.  
 TITLE Coding sequence of human placenta coffilin cdna  
 JOURNAL Nucleic Acids Res. 18 (23), 7169 (1990)  
 MEDLINE 91088330  
 COMMENT These data kindly submitted in computer readable form by: Kazuo Ogawa  
 The 1st deviation, Dep. of Int. Med.  
 Fukushima Medical College  
 1-Hikarigaoka  
 Fukushima 960  
 Japan  
 Phone: 0245-48-2111.  
 Location/Qualifiers  
 1..501  
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BASE COUNT 128 a 119 c 156 g 98 t  
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 Ratio: 1.762 Gaps: 7  
 Percent Similarity: 64.458 Percent Identity: 30.120

alignment\_block:

US-09-722-838-2 x HUMCOF ..

Align seg 1/1 to: HUMCOF from: 1 to: 501

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1 ATGGCTCCGGTGGCTGCTCTCATGATGTCATCAAGGTGCTCAACGA 50
  ::::::::::::::::::::::::::::||| ::::::::::::::
19 pPheArgMetSerGlyAsnLysAla.....AsnLysThrL 31
  ::::::::::::::::::::::::::::||| ::::::::::::::
51 CATGAAGGTGCTTAAGTCTTCAAGCCAGAGAGAGTGAAGAGCCGCA 100
  ::::::::::::::::::::::::::::||| ::::::::::::::
31 ySPheIleIlePheLysIleAlaAspAsnLysLysGluValAlaIleAsp 47
  ::::::::::::::| ::::::::::::::| ::::::::::::::|
101 AGCGGCTGCTCTTCTGCTGAGTGAAGCAAGAACATCATCTCTGGAG 150
  ::::::::::::::| ::::::::::::::| ::::::::::::::|
48 Glu.....ValSerGln.....GluGlnAs 54
  ::::::::::| ::::::::::| ::::::::::|
151 GAGGGCAAGAGATCCTGATGGCGATGTGGCGCACTGTCGACGATCC 200
  ::::::::::| ::::::::::| ::::::::::|
54 pTyGluValAlaPheArgSerArgLysGluAlaThrLysAspSerLysGly 71
  ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
201 CTACGCCACCTTGTCAAGATGCTG...CCAGATTAAGGACTGC..... 240
  ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
71 snProAlaProArgTyrAlaValTyrAspValGluTyrAspLysGly 87
  ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
241 .....CGTATGCCCTCTATGATGCAACTATGAGACC..... 273
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88 GlyGluGlyLysArgSerLysIleValPheIleSerTyrValProSerAs 104
  ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
274 AAGGAGACCAAGAGAGATCTGCTGTATCTTCTGGCCGCCGAGAGTC 323
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104 pThrProThrLeuTyrPseMetIleTyrAlaSerThrArgGluAsnLeu 121
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324 TGGCCGCCCTTAAGACCAAAATGATTATTCAGCTCAAGAGCCCATCA 373  
 121 yASnAlaLeu...AsnIleHstHrSerIleHlaAlaAspLysGly 136  
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 374 AAGAGAGCTGACAGGATCAAGATGAATTCAGCAAGCAAACTGACAG 423  
 137 AspIleGluTyrThrValLeuAlaGluAlaSerGlyGlyAla 152  
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seq\_documentation\_block:

LOCUS HSU21909 960 bp mRNA PRI 29-MAR-1995  
 DEFINITION Human cofilin mRNA, partial cds.  
 ACCESSION U21909  
 VERSION U21909.1 GI:736399  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (sites)

REFERENCE 1  
 AUTHORS Van der Steege, G., Draaijers, T.G., Grootsohollen, P.M., Oslinga, J., Buys, C.H.C.M., Anzevin, R., Velone, I., Brahe, C., Scheffer, H., Van Ommen, G.J.B. and

TITLE A provisional transcript map of the spinal muscular atrophy (SMA)

REFERENCE 2 (bases 1 to 960)  
 TITLE Direct Submission  
 JOURNAL Submitted (28-FEB-1995) Gerrit Van der Steege, University of Groningen, Department of Medical Genetics, Antonius Deusinglaan 4, Groningen, 9713 AW, The Netherlands

FEATURES  
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 LEGRPL"

CDS

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 Quality: 188.50 Length: 166  
 Ratio: 1.762 Gaps: 7  
 Percent Similarity: 64.458 Percent Identity: 30.120

alignment\_block:

US-09-722-838-2 x HSU21909 ..

Align seg 1/1 to: HSU21909 from: 1 to: 960

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3 LeuAlaSerGlyValSerIleAlaAspGluCysIleThrAlaPheAsnAs 19
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1 ATGGCTCCGGTGGCTGCTCTCATGATGTCATCAAGGTGCTCAACGA 50
  ::::::::::::::::::::::::::::||| ::::::::::::::
19 pPheArgMetSerGlyAsnLysAla.....AsnLysThrL 31
  ::::::::::::::::::::::::::::||| ::::::::::::::

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MEDLINE 96393663  
 REFERENCE 2 (bases 1 to 1059)  
 AUTHORS Gillett, G.T.  
 TITLE Direct Submission  
 JOURNAL Submitted (27-JAN-1996) G.T. Gillett, GOS Hospital NHS Trust,  
 Clinical Biochemistry, Great Ormond Street, London, WC1N 3JH, UK

FEATURES  
 source location/Qualifiers  
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 /note="induced with DMSO"  
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 /db\_xref="GI:1177471"  
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 LEGRPL"

gene  
 CDS  
 polyA\_signal 941..946  
 BASE COUNT 220 a 311 c 282 g 246 t  
 ORIGIN

alignment\_scores:  
 Quality: 188.50 Length: 166  
 Ratio: 1.762 Gaps: 7  
 Percent Similarity: 64.458 Percent Identity: 30.120

alignment\_block:  
 US-09-722-838-2 x HSNMCF1 ..

Align seg 1/1 to: HSNMCF1 from: 1 to: 1059

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|||||
52 ATGGCTCCGGTGGTCTCTGTCATGTCATCAAGGTCATCAACGA 101
|||||
19 pPheArgMetSerGlyAsnLysAla.....AsnLysThrL 31
|||||
102 CATGAAGGTGCGTAAGTCTCAACGCCAGAGAGGTGAAGAACGCCAAGA 151
|||||
31 ySPheIleIlePheLysIleAlaAspAsnLysLysGluValAlaIleAsp 47
|||||
152 AGCGGCTGCTCTTCTGCGTGAAGTGAAGCAACATCATCTCGAGG 201
|||||
48 Glu.....ValSerGln.....GluGluAs 54
|||||
202 GAGGGCAAGAGATCCTGTCGCGCATGTCGACACTGTCGACAGATCC 251
|||||
54 pTyrcIuValAlpHeArgSerArgLysGluAlaThrLysAspSerLysGly 71
|||||
252 CTACGCCCACTTTGTCAAGATCTG...CCAGATTAAGGCTCC..... 291
|||||
71 snProAlaProArgTyrAlaValTyrAspValGluTyrAspLysGly 87
|||||
292 .....CGCTATGCCCTCTATGATGCAACCTATGAGACC..... 324
|||||
88 GlyGluGlyLysArgSerLysIleValPheIleSerTyrPvalProSerAs 104
|||||
325 AAGGAGACCAAGAGAGATCTGCTTATCTCTGCGCCCGCAGAGTC 374
|||||
104 pThrProThrLeuTrpSerMetIleTyrAlaSerThrArgGluAsnLeuL 121

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375 TCGGCCCTTAAGACCAAAATGTTTATCCACCTCCAGAGCCCATCA 424
|||||
121 yAsnAlaLeu...AsnIleHisThrSerIleHisAlaAspAspLysGly 136
|||||
425 AGAAGAGCTGACAGGATCAAGCATGATGCAACCAACGTCATGACAG 474
|||||
137 AspIleGluTrpLysThrValLeuAlaGluAlaSerGlyLysAla 152
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475 GAGGTCAAGACCGCTGCACCTGCGCAGAGACTGGGGCGATCGG 522
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seq_name: gb:BC011005
seq_documentation_block:
LOCUS BC011005 1086 bp mRNA PRI 25-JUL-2001
DEFINITION Homo sapiens, similar to cofilin 1, non-muscle, clone MGC:16554
IMAGE:4079579, mRNA, complete cds.
ACCESSION BC011005
VERSION BC011005.1 GI:15012200
KEYWORDS MGC.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1086)
Strausberg, R.
REFERENCE Direct Submission
AUTHORS Submitted (23-JUL-2001) National Institutes of Health, Mammalian
TITLE Gene Collection (MGC), Cancer Genomics Office, National Cancer
JOURNAL Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.ncl.nih.gov
COMMENT Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbio.org
contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Kettelman and Anuradha Madan
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 25 Row: O Column: 22.
location/Qualifiers
1..1086
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MGC:16554 IMAGE:4079579"
/tissue_type="uterus, leiomyosarcoma"
/clone_id="NIH-MGC-46"
/lab_host="DH10B-R"
/note="vector: pOTB7"
72..572
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/product="Similar to cofilin 1, non-muscle"
/protein_id="AAH11005.1"
/db_xref="GI:15012201"
/translation="MASGVAVSDGVIRKVFNDMKVRKSTPEEYKKRKAIVFLCSEDK
KNILLEGKELIVDGQYDDPYATFVKMLPKDCRYALYDAITYETKESKKEDLVFI
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LEGRPL"


BASE COUNT 231 a 318 c 292 g 245 t  

  ORIGIN



alignment_scores:  

  Quality: 188.50 Length: 166  

  Ratio: 1.762 Gaps: 7  

  Percent Similarity: 64.458 Percent Identity: 30.120


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## alignment\_block:

US-09-722-838-2 x BC011005 ..

Align seg 1/1 to: BC011005 from: 1 to: 1086

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3 LeuAlaSerGlyValSerIleAlaAspGluCysIleThrAlaPheAsnAs 19
  ::::::::::::::::::::::::::::::::::::::::::::::::::::
72 ATGGCTCCGGTGGCTGCTCTGTGATGCTGTCATCAAGGTCTCAACGA 121
  ::::::::::::::::::::::::::::::::::::::::::::::::::::
19 pPheArgMetSerGlyAsnLysAla.....AsnLysThrL 31
  ::::::::::::::::::::::::::::::::::::::::::::::::::::
122 CATGAAGGTGGCTAAGTCTTCAAGCCAGAGAGAGTCAAGAGCCAGAGA 171
  ::::::::::::::::::::::::::::::::::::::::::::::::::::
31 yspPheIleIlePheLysIleAlaAspAsnLysGluValIleAsp 47
  ::::::::::::::::::::::::::::::::::::::::::::::::::::
172 AGGGCGGTGCTCTGCTGCTGATGAGCAAGAAAGACATCATCTGGAG 221
  ::::::::::::::::::::::::::::::::::::::::::::::::::::
48 Glu.....ValSerGln.....GluGluAs 54
  ::::::::::::::::::::::::::::::::::::::::::::::::::::
222 GAGGGCAAGAGATCCGTGGGCGATGTGGCCAGACTGTGCGAGATCC 271
  ::::::::::::::::::::::::::::::::::::::::::::::::::::
54 pTYrGluValPheArgSerArgLeuGluAlaThrLysAspSerLysGly 71
  ::::::::::::::::::::::::::::::::::::::::::::::::::::
272 CTAGCCACCTTGTCAAGATGCTG...CCAGATAAGACTGC..... 311
  ::::::::::::::::::::::::::::::::::::::::::::::::::::
71 snProAlaProArgTYrAlaValTYrAspValGluTYrAspLeuGly 87
  ::::::::::::::::::::::::::::::::::::::::::::::::::::
312 .....CGCTATGCCCTCTATGATGCAACCTATGAGACC..... 344
  ::::::::::::::::::::::::::::::::::::::::::::::::::::
88 GlyGluGlyLysArgSerLysIleValPheIleSerThrValProSerAs 104
  ::::::::::::::::::::::::::::::::::::::::::::::::::::
345 AAGGAGAGCAAGAAAGAGATGTGCTTATCTTCTGGCCCGCAGATC 394
  ::::::::::::::::::::::::::::::::::::::::::::::::::::
104 pThrProThrLeuTrpSerMetIleTYrAlaSerThrArgLysLeuL 121
  ::::::::::::::::::::::::::::::::::::::::::::::::::::
395 TGGCCCTTAAAGAGCAAAATGATTATCCAGCTCAAGAGCCAGCA 444
  ::::::::::::::::::::::::::::::::::::::::::::::::::::
121 ysnAlaLeu...AsnIleHisThrSerIleHisAlaAspLysGly 136
  ::::::::::::::::::::::::::::::::::::::::::::::::::::
445 AGAAGAGAGCTGACAGGATCAAGCATGATTCAGAACCAACGCTACAG 494
  ::::::::::::::::::::::::::::::::::::::::::::::::::::
137 AspIleGluTrpLysThrValLeuAlaGluAlaSerGlyGlyLysAla 152
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495 GAGGTCAGAGACCGCTGCACCTGCGAGAGAAAGTGGGGCGAGATGCC 542
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seq\_name: gb.pr:BC012265

seq\_documentation\_block:

LOCUS BC012265 1098 bp mRNA PRI 08-AUG-2001  
 DEFINITION Homo sapiens, similar to cofillin 1, non-muscle, clone MGC:9272  
 IMAGE:3862540, mRNA, complete cds.  
 ACCESSION BC012265  
 VERSION BC012265.1 GI:15126675  
 KEYWORDS MGC.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 1098)  
 AUTHORS Strausberg, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (06-AUG-2001) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA  
 NIH-MGC Project URL: <http://mgc.ncl.nih.gov>  
 Contact: MGC help desk  
 Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
 Tissue Procurement: DCTD/DPF  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Baylor College of Medicine Human Genome  
 Sequencing Center

REMARK COMMENT

Center code: BCM-HGSC  
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
 Contact: [villaloboscm.tmc.edu](mailto:villaloboscm.tmc.edu)  
 Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,  
 A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,  
 Muzny, D.M., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAC Plate: 21 Row: 9 Column: 21  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: Hexamer frequency ORF  
 analysis, similarity but not identity to protein.  
 Location/Qualifiers  
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 /db\_xref="taxon:9606"  
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 /tissue\_type="Ovary, adenocarcinoma"  
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 /lab\_host="DH10B"  
 /note="Vector: pCMV-SPORT6"  
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 LEGKPL"

## CDS

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BASE COUNT      244 a      318 c      289 g      247 t
ORIGIN

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alignment\_scores:  
 Quality: 188.50 Length: 165  
 Ratio: 1.762 Gaps: 7  
 Percent Similarity: 64.458 Percent Identity: 30.120

alignment\_block:

US-09-722-838-2 x BC012265 ..

Align seg 1/1 to: BC012265 from: 1 to: 1098

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  ::::::::::::::::::::::::::::::::::::::::::::::::::::
68 ATGGCTCCGGTGGCTGCTCTGTGATGCTGTCATCAAGGTCTCAACGA 117
  ::::::::::::::::::::::::::::::::::::::::::::::::::::
19 pPheArgMetSerGlyAsnLysAla.....AsnLysThrL 31
  ::::::::::::::::::::::::::::::::::::::::::::::::::::
118 CATGAAGGTGGCTAAGTCTTCAAGCCAGAGAGAGGTGAAGAACCCAGAGA 167
  ::::::::::::::::::::::::::::::::::::::::::::::::::::
31 yspPheIleIlePheLysIleAlaAspAsnLysGluValIleAsp 47
  ::::::::::::::::::::::::::::::::::::::::::::::::::::
168 AGCGGTGCTCTTGTGCTGATGAGCAAGAAAGACATCATCTCTGGAG 217
  ::::::::::::::::::::::::::::::::::::::::::::::::::::
48 Glu.....ValSerGln.....GluGluAs 54
  ::::::::::::::::::::::::::::::::::::::::::::::::::::
218 GAGGGCAAGAGATCCGTGGGCGATGTGGCCAGACTGTGCGAGATCC 267
  ::::::::::::::::::::::::::::::::::::::::::::::::::::
54 pTYrGluValPheArgSerArgLeuGluAlaThrLysAspSerLysGly 71
  ::::::::::::::::::::::::::::::::::::::::::::::::::::
268 CTAGCCACCTTGTCAAGATGCTG...CCAGATAAGACTGC..... 307
  ::::::::::::::::::::::::::::::::::::::::::::::::::::
71 snProAlaProArgTYrAlaValTYrAspValGluTYrAspLeuGly 87
  ::::::::::::::::::::::::::::::::::::::::::::::::::::
308 .....CGCTATGCCCTCTATGATGCAACCTATGAGACC..... 340
  ::::::::::::::::::::::::::::::::::::::::::::::::::::
88 GlyGluGlyLysArgSerLysIleValPheIleSerThrValProSerAs 104
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seq_name= gb_pr:BC012318

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LOCUS      BC012318              1105 bp          mRNA                PRI       10-AUG-2001
DEFINITION Homo sapiens, Similar to cofilin 1, non-muscle, clone MGC:15952
IMAGE:3538185, mRNA, complete cds.
ACCESSION   BC012318
VERSION     BC012318.1    GI:15147368
KEYWORDS    MGC.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mamalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 1105)
AUTHORS     Strauberg,R.
TITLE       Direct Submission
JOURNAL     Submitted (09-AUG-2001) National Institutes of Health, Mammalian
Genetic Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK      NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
Email: cgapbs@email.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@cgsc.bc.ca
Suzanne Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Steven Chan, Readman Chin, Chris Fjell, Erin Gardlan, Ran Guin, Letticia Hsiao, Martin Krywinski, Reta Kusche, Oliver Lee, Soo Sen Dee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Lissa Prabhu, Parvaneh Saeedi, Jacqueline Schehl, Duane Smalusz, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.llnl.gov Series: IRAL.Plate: 23 Row: k Column: 15 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.

FEATURES             SourceQualifiers
Location/Qualifiers
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         /lab_host="DH10B-R"
         /note="Vector: pOT87"
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```

```

BASE COUNT      248 a      318 c      290 g      249 t      LEGRPL"
ORIGIN
alignment_scores:
    Quality: 188.50      Length: 166
    Ratio: 1.762      Gaps: 7
    Percent Similarity: 64.458      Percent Identity: 30.120
alignment_block:
US-09-722-838-2 x BC012218 ..
Align seg 1/1 to: BC012218 from: 1 to: 1105
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67 ATGGCGCTCCGGTGTGCTGTCTGTGATGCTGATCAACAGGTTCACAGA 116
19 pheArgMetSerGlyAsnLyAla.....AsnLySThL 31
1:::|||||:::|||||:::|||||:::|||||
117 CATGAAGGGTGGCTAAGCTTCAACGCCAGAGAGAGCTGAAGAAAGCGAGA 166
31 yspHelIlePheLysIleAlaAspAsnLyLysGluValValIleAsp 47
||:::|||||:::|||||:::|||||:::|||||
167 AGCGCGTCTCTTCTGCTGAGTGAAGACAAAGAACATCATCTCTGGAG 216
48 Glu.....ValSerGln.....GluGlnAs 54
||:::|||||:::|||||:::|||||
217 GAGGCGCAAGAGATCCTGGTGGCGATGTGGGCGCAAGCTGTGACAGATCC 266
54 pyrGluValPheArgSerArgLeuGluAlaThrLysAspSerLyGlyA 71
||:::|||||:::|||||:::|||||:::|||||
267 CTACGCCACCTTGTCAAGAGTCTG...CCAGATAAAGGACTCC..... 306
71 snProAlaProArgTyrAlaValTyrAspValGluTyrAspLeuGly 87
|||:::|||||:::|||||:::|||||:::|||||
307 .....CGCTATGCCCTCTATGATGCAACCTATGAGACC..... 339
88 GlyGluGlyLysArgSerLysIleValPheIleSerTyrPvalProSerAs 104
|||:::|||||:::|||||:::|||||:::|||||
340 AAGGAGAGCAAGAGAGAGATGTGGGTATCTTCTGTGGCCCCCGAGAGC 389
104 pthrProThrLeuTyrPserMetIleTyrLaseThrArgLysuanLeuL 121
390 TCGCGCCCTTAAAGACCAAAATGATTTATGCCCAGCTCCAAAGAGCCCATCA 439
121 yAsnAlaLeu...AsnIleHsThrSerIleHsAlaAspAspLyGly 136
||:::|||||:::|||||:::|||||:::|||||
440 AAGAGAGCTGACAGGAGATCAAGCATGATTCGACCAACATCGCTACGAG 489
137 AspIleGluTyrLysThrValLeuAlaGluAlaSerGlyGlyLysAla 152
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490 GAGGTCAAGGACCGCTGACACCTCGAGAGAGAAAGTGGGGGAGTGGCC 537
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seq_documentation_block:
LOCUS      BC011444      1131 bp      mRNA      PRI      30-JUL-2001
DEFINITION Homo sapiens, coffin 2 (muscle), clone MGC:13364 IMAGE:4245104,
ACCESSION      BC011444
VERSION      BC011444.1 GI:15030331
KEYWORDS      MGC.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS      Strausberg,R.
TITLE      Submitted (25-JUL-2001) National Institutes of Health, Mammalian
JOURNAL      Gene Collection (MGC), Cancer Genomics Office, National Cancer

```



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LECKPL"

BASE COUNT 881 a 485 c 552 g 991 t  
ORIGIN

alignment\_scores:  
Quality: 188.50 Length: 164  
Ratio: 1.812 Gaps: 6  
Percent Similarity: 63.415 Percent Identity: 29.268

alignment\_block:  
US-09-722-838-2 x BC007138 ..

Align seg 1/1 to: BC007138 from: 1 to: 2909

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75 AAGGATCTCGAGTACAGTGAATGATGAAATCAAAAGTTTAAATGA 124
  |::::::::::::::::::|
19 pPheArgMetSerGlyAsnLysAla.....AsnLysThrL 31
  |::::::::::::::::::|
125 TATGAAAGTAAAGAAATCTTCTACACAGAGAGAGATCAAAAAGAAAGA 174
  |::::::::::::::::::|
31 ySPheIleIlePheLysIleAlaAspAsnLysLysGluValIleAsp 47
  || ::::::::::| ::::::::::| ::::::::::| ::::::::::|
175 AAGCAGTCTCTCTGTTGTTGACGATGACAAAGAACAAATATTTGAGAG 224
  ||::::::::::::::::::|
48 GluValSerGln.....GluGlnAs 54
  ||::::::::::::::::::|
225 GAAGCCAGACAGATCTGTGGTGACATTTGGTACACTGTAGAGAGACC 274
  |||
54 pTyrGluValPheArgSerArgLeuGluAlaThrLysAspSerLysGlyA 71
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275 CTACACATCTTT...GTGAAGTTGCTTACCTCTGAAATGATGTC..... 314
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71 snProAlaProArgTyrAlaValTyrAspValGluTyrAspLeuGlyGly 87
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315 .....CGATATGCTTGTACGATGCCACATACGAACA..... 347
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88 GlyGluGlyLysArgSerLysIleValPheIleSerTrpValProSerAs 104
  ||| ::::::::::| ::::::::::| ::::::::::|
348 AAAGAGTCTAAGAAAGAACCTAGTATTATTTCTGGGCTCTGAAG 397
  |||
104 pThrProThrLeuTrpSerMetIleTyrAlaSerThrArgGluAsnLeuL 121
  ::::::::::|
398 TGCACCGTTAAAGAAAGATGATTATGCTAAGATGCCATTGA 447
  ::::::::::|
121 yAsnAlaLeu...AsnIleHisThrSerIleHisAlaAspAspLysGly 136
  ||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
448 AAAAGAAATTTACAGTATTAACAATGAGTGCAAGTAAATGCTTGAGC 497
  |||
137 AspIleGluTrpLysThrValLeuAlaGluAlaSerGlyGly 150
  ||| ::| ::| ::| ::| ::| ::| ::| ::| ::|
498 GATTATTAAAGACCGCTCGACGCTGGGAGAGAAACTGGGGGC 539
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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

# OM protein - protein search, using sw model

Run on: January 29, 2002, 18:16:47 ; Search time 735.43 Seconds  
(without alignments)  
30.630 Million cell updates/sec

Title: US-09-722-838-2  
Perfect score: 796  
Sequence: 1 MALASGVIADECTAFNDF.....KGDIEKTYLAASGKAGK 154

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues  
Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mhc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp.rodent:\*  
12: sp.virus:\*  
13: sp.vertebrate:\*  
14: sp.unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	276	34.7	156	3 005307	005307 saccharomyc
2	274	34.4	143	3 09HP97	09HP97 zygosacchar
3	192.5	24.2	142	10 043655	043655 tritilicum ae
4	186.5	23.4	229	11 09CX22	09CX22 mus musculus
5	183.5	23.1	144	10 09FEC6	09FEC6 lophopyrum
6	178	22.4	143	10 09FVII	09FVII petunia hyb
7	177	22.2	139	10 039250	039250 arabidopsis
8	173	21.7	140	10 09LQ81	09LQ81 arabidopsis
9	171	21.5	139	10 09FVII2	09FVII2 petunia hyb
10	169	21.2	138	10 09XEN2	09XEN2 zea mays (m
11	169	21.2	139	10 09FJ7	09FJ7 arabidopsis
12	167.5	21.0	139	10 09SK3	09SK3 arabidopsis
13	164	20.6	139	10 09SK2	09SK2 zea mays (m
14	162	20.4	146	10 09SK4	09SK4 arabidopsis
15	158	19.8	139	10 09M54	09M54 elaeis guin
16	158	19.8	140	10 09AY76	09AY76 oryza sativ
17	156	19.6	145	10 09FWC0	09FWC0 oryza sativ
18	155	19.5	153	10 09FWC0	09FWC0 oryza sativ
19	155	19.5	153	10 09FWC0	09FWC0 oryza sativ

20	152	19.1	132	10 09SJX6	09SJX6 arabidopsis
21	152	19.1	137	10 039251	039251 arabidopsis
22	151	19.0	130	10 09FWC4	09FWC4 arabidopsis
23	150.5	18.9	293	5 09UAV4	09UAV4 caenorhabd
24	150	18.8	130	10 065603	065603 arabidopsis
25	150	18.8	165	11 09R0P5	09R0P5 mus musculi
26	149.5	18.8	143	10 09ZWT3	09ZWT3 arabidopsis
27	148.5	18.7	129	10 09SM69	09SM69 malus domes
28	145	18.2	133	10 065277	065277 arabidopsis
29	144.5	18.2	133	10 09L7R3	09L7R3 arabidopsis
30	140	17.6	118	5 015902	015902 toxoplasma
31	140	17.6	132	10 09SLE7	09SLE7 arabidopsis
32	138	17.3	130	10 09L7R2	09L7R2 arabidopsis
33	123	15.5	130	10 049606	049606 arabidopsis
34	114	14.3	141	3 013808	013808 schistosach
35	112	14.1	148	5 09VWRI	09VWRI drosophila
36	100	12.6	328	3 094399	094399 schizosach
37	97	12.2	138	5 09NK59	09NK59 drosophila
38	97	12.2	141	5 09VJL6	09VJL6 drosophila
39	95	11.9	350	4 012792	012792 homo sapien
40	93.5	11.7	149	3 012156	012156 saccharomyc
41	93	11.7	350	11 009132	009132 mus musculi
42	90.5	11.4	414	2 09L7R8	09L7R8 salmoneilla
43	83	10.4	142	11 09L7R8	09L7R8 mus musculi
44	83	10.4	142	13 09L7R6	09L7R6 cyprinus ca
45	83	10.4	154	4 09BS35	09BS35 homo sapien

## ALIGNMENTS

RESULT 1  
ID 005307 PRELIMINARY; PRT; 156 AA.  
AC 005307;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE ORF L0596.  
GN COF1 OR YL050C.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=S288C;  
RA Medler H., Mambuli R.;  
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Z47973; CAAB8007.1; -.  
DR HSSP; Q03048; ICOF.  
DR SGD; S0003973; COF1.  
DR InterPro; IPR002108; Cofilin\_ADF.  
DR Pfam; PF00241; Cofilin\_ADF; 1.  
DR ProDom; PD002129; Cofilin\_ADF; 1.  
DR SMART; SM0102; ADF; 1.  
DR PROSITE; PS00325; ACTIN\_DEPOLYMERIZING; 1.  
SQ SEQUENCE 156 AA; 17566 MW; E773F019BE04DE55 CRC64;

Query Match 34.7% Score 276; DB 3; Length 156;  
Best Local Similarity 38.3% Pred. No. 8e-18;  
Matches 57; Conservative 27; Mismatches 45; Indels 20; Gaps 4;  
QY 7 VSIDECTAFNDFRMGKANKRTKFTFKIADKKKEVIDEVSQEDYEFRRSLBATK 66  
DB 19 YVAVDESLTAFNDKLT-----CKKTKFTFLGLNDAKTEIVAKETSTDSYDALEKLT----- 70  
QY 67 DSKGNPAFR---YAVYDVEYDGLGGGGRSKRIVFISWVPSDPTLMSIYASTRENLIK 122  
DB 71 -----PNDCLTVAIYDFEYEINGEGRKRIKIVFTWSPDTATVRKMKVYASSKDALRR 123  
QY 123 ALN-IHSHADDKGDIEMKTYLAASG 150

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Db      124  ALNGVSTDYOGTFDESEVSYSLVERYSRG 152
RESULT      2
O9HF97      PRELIMINARY;      PRT;      143 AA.
AC      O9HF97;
DT      01-MAR-2001 (TREMblrel, 16, Created)
DT      01-MAR-2001 (TREMblrel, 16, Last sequence update)
DT      01-JUN-2001 (TREMblrel, 17, Last annotation update)
DE      COFILIN.
GN      COF1.
OS      Zygosaccharomyces rouxii (Candida mogii).
OC      Eukaryota: Fungi: Ascomycota: Saccharomycotina: Saccharomycetes;
OC      Saccharomycetales; Saccharomycetaceae; Zygosaccharomyces.
OX      NCBI_TaxID=4956;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Suda A., Nakagawara H., Kusama K., Ogawa Y., Watanabe K.;
RT      "Role of cof1lin on actin dynamism in Zygosaccharomyces rouxii.",
RL      Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
DR      EMBL; AB052106; BAB18899.1; -.
DR      InterPro: IPR002108; Cofilin_ADF.
DR      Pfam: PF00241; cofilin_ADF.1.
DR      ProDom: PD002129; cofilin_ADF.1.
DR      SMART: SM00102; ADF.1.
DR      PROSITE: PS00325; ACTIN_DEPOLYMERIZING.1.
SO      SEQUENCE 143 AA; 15882 MW; F0C5BC3679DEED42 CRC64;

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Query Match	34.48;	Score 274;	DB 3;	Length 143;
Best Local Similarity	37.68;	Pred. No. 1.1e-17;		
Matches	56;	Conservative	30;	Mismatches 43;
			Indels	20;
			Gaps	4

[illegible]

RESULT	3			
ID	043655	PRELIMINARY;	PRT;	142 AA.
AC	043655;			
DT	01-NOV-1996 (TrEMBLrel. 01, Created)			
DT	01-NOV-1996 (TrEMBLrel. 01, last sequence update)			
DT	01-JUN-2001 (TrEMBLrel. 17, last annotation update)			
DE	WCOR719.			
GN	WCOR719.			
OS	Triticum aestivum (wheat).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; Poideae			
OC	Triticeae; Triticum.			
OX	NCBI_TaxID:4565;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	SPRAIN-CV. NORSTAR. TISSUE=SEEDLING SHOOT;			
RX	MEDLINE-96335619; PubMed-8766725;			
RA	Danyuk J., Carpentier E., Sarhan F.;			
RT	"Identification and characterization of a low temperature regulated			
RL	gene encoding an actin-binding protein from wheat.";			
FT	FEBS Lett. 389:324-327(1996).			
DR	EMBL: U58278; AAC49404.1; -			
DR	HSSP: P37167; ICNU.			
DR	Mendel; 10853; Triae;1044;10853.			

DR InterPro: IPR002108; Cofilin\_ADF.  
DR Pfam: PF00241; cofilin\_ADF, 1.  
DR ProDom: PD002129; Cofilin\_ADF, 1.  
DR SMART: SM00102; ADF, 1.  
SQ SEQUENCE 142 AA; 15764 MW; D06F2F0C8DB5C18 CRC64;

Query Match	24.2%;	Score 192.5;	DB 10;	Length 142;
Best Local Similarity	31.9%;	Pred. No. 3.1e-10;		
Matches 45;	Conservative 28;	Mismatches 47;	Indels 21;	Gaps 5

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QY 5 GSGVSIADCCIAFNFDFRSGNKAHKTFFIIFKIDNKEVIVDEVSQEDYEWFRLSLTA 64
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 6 SGVAVNECECVAFQELRAE-----KKHRRVYVYKKMDAQVYVYDKV-----GALDA 51

QY 65 TKDSKGNAP-----RYAVYDEY--DLGGGGRKSKIVYFSWPSDPTILMSIYASTRE 118
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 52 TFDLLAAMPDDCRITAYVYDDVSEDSAGGTPTPSKIFLTHMSESDADANKKILYASTE 111
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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QY      119 NKNALN-IHTSIHADKDI 138
          | | : : | | : :
Db      112 GLKKELDVQIDVQATDASEL 132

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RESULT	4
Q9CX22	
ID	Q9CX22
	PRELIMINARY;
	PRT; 229 AA

DT 01-JUN-2001 (TREMBLrel. 17, created)  
DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)  
DE COFILIN 1, NON-MUSCLE.  
GN CFL1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus  
OX NCBI\_TaxID=10090;  
NN [1]

RC STRAIN=C57BL/6J;  
RC TISSUE=EMBRYONIC BODY BETWEEN DIAPHRAGM REGION, AND NECK;  
RX MEDLINE=21085660; Pubmed=11217851;  
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishi Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Gotohori T., Bono H., Kasukawa T., Saito R.,  
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Koehli A.H.,  
RA Kiehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schirral L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Gromstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustinovich S., Hill D., Hofmann M., Hume D.A., Kamlya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli U., Momberts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitteker C., Wilmink L.,  
RA Wyusluh-Borits A., Yoshida K., Hasegawa Y., Kawai H., Kotsuki S.,  
RA Hayashizaki Y.;  
RT "functional annotation of a full-length mouse cdna collection.";  
RL Nature 409:685-690(2001).  
DR EMBL: AK020471; BAB32114.1; -.  
DR MGD: MGI:101757; Cfll1.  
DR InterPro: IPR002108; CoFilin\_ADF.  
DR Pfam: PF00241; cofilin\_ADF.1.  
DR PRINTS: PR00006; COFILIN.  
DR ProDom: PD002129; cofilin\_ADF.1.  
DR SMART: SM00102; ADF.1.  
DR PROSITE: PS00325; ACTIN\_DEPOLYMERIZING.1.  
QO SCQUENCE 229 AA; 24796 MW; 1198EEA88E16B75 CRC64;

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Query Match          23.4%; Score 186.5; DB 11; Length 229;
Best Local Similarity 30.1%; Pred. NO. 2e-09;
Matches 50; Conservative 34; Mismatches 57; Indels 25; Gaps
7;

QY 3 LAGSVIDECTTANFDRMSGNKA-----NKTKEIFIKIADNKKKEVIDE-----V 49
   |||||:| | | | : : : : | : | : | : | : | : | : | : | : |
Db 1 MASSGAAVSDGYATKYVNDKMRKRSSTPEEVKKRKKKAVCLSDKNNIILEEKEILLGV 60
   : : : : | : | | : | : | : | : | : | : | : | : | : | : |

QY 50 SQ--EDDYEVFRSRLKATKDSKGNPAPRYAVYDVEYDLGGGEGSKRSKIVFISWPSDPT 107
   : : : : | : | | : | : | : | : | : | : | : | : | : | : |
Db 61 GOTVDDPYTTFVKML-PKXDC-----RYALDVAIYET--KRSKKEDLVFIWAPENAPL 111
   ' : : : : | : | | : | : | : | : | : | : | : | : | : | : |

QY 108 LMSMTYASTRENLKAL-NHTSHADDKGDIEMKTVLAEASGGA 152
   |||||:| | | | : : : : | : | : | : | : | : | : | : | : |
Db 112 KSMKIYASSKDAIKKKTGKIKHELOANCYEKVKDCRTIAEKLGGA 157
   ' : : : : | : | | : | : | : | : | : | : | : | : | : | : |

RESULT 5
Q9FEC6 PRELIMINARY; PRT; 144 AA.
AC Q9FEC6;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE ACTIN DEPOLYMERIZATION FACTOR-LIKE PROTEIN.
GN ES128.
OS Lophopyrum elongatum ('Tall wheatgrass') (Argopyrum elongatum).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Lophopyrum.
OX NCBI_TaxID=4588;
RN [1]
RP SEQUENCE FROM N.A.
RA Gulick P.J., Dvorak J.;
RT "Coordinate gene response to salt stress in Lophopyrum elongatum.";
RL Plant Physiol. 100:1384-1388(1992).
RN [2]
RP SEQUENCE FROM N.A.
RA Abu-Idrees A., Shen W., Gulick P.J.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Abu-Idrees A., Shen W., Gulick P.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF196350; AAC28490.1; -.
DR EMBL: AF195612; AAC28460.1; -.
DR InterPro: IPR002108; COG11n_ADF.
DR Pfam: PF00241; COG11n_ADF.1.
DR ProDom: PD002129; COG11n_ADF.1.
DR SMART: SM00102; ADF.1.
SQ SEQUENCE 144 AA; 15953 MM; 3D6CE2039FD698FC CRC64;

Query Match          23.1%; Score 183.5; DB 10; Length 144;
Best Local Similarity 31.5%; Pred. No. 2.1e-09;
Matches 45; Conservative 29; Mismatches 46; Indels 23; Gaps
6;

QY 5 SGVSIADECTAANFDRMSGKANNTKTFIFIAANK--KEVVIDEVSQEDIEVFRSRL 62
   |||||:| | | | : : : : | : | : | : | : | : | : | : | : |
Db 6 SGVAANECCVAFQELRAE-----RKHREYVYTKMDDDEDAQOYVADKV-----GAL 51
   : : : : | : | | : | : | : | : | : | : | : | : | : | : |

QY 63 EATKDSKGNPAP---RAVYDVEY--DLGGEGSKRSKIVFISWPSDPTLMSNIYAST 116
   : : : : | : | | : | : | : | : | : | : | : | : | : | : |
Db 52 DATFDLAAAMPADDCRAVYDLDVSDSDAGDPTFRSKITFIWSPALADARSKNVIYASS 111
   : : : : | : | | : | : | : | : | : | : | : | : | : | : |

QY 117 RBNLKNALN-IHTSHADKGD 138
   | | | : : | : | : :
Db 112 TEGLKKELDGVOIDVQATDASEL 134
   | | | : : | : | : :

RESULT 6
Q9FVII PRELIMINARY; PRT; 143 AA.
ID Q9FVII

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AC      09EV11:
DT      01-MAR-2001 (TREMBlrel. 16, Created)
DT      01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT      01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE      ACTIN-DEPOLYMERIZING FACTOR 2.
GN      ADF2.
OS      Petunia hybrida (Petunia).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC      Asteridae; euasterids I; Solanales; Solanaceae; Petunia.
OX      NCBI_TaxID=4102;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      PubMed=11080583;
RA      Mun J.H., Yu H.J., Lee H.S., Kwon Y.M., Lee J.S., Lee I., Kim S.G.;
RT      "Two closely related cDNAs encoding actin-depolymerizing factors of
RL      Petunia are mainly expressed in vegetative tissues.";
RL      Gene 257:167-176(2000).
DR      EMBL; AF183904; AAG16974.1; -
DR      InterPro; IPR002108; Cofilin_ADF.
DR      Pfam; PF00241; cofilin_ADF.1.
DR      PRINTS; PR00006; COFILIN.
DR      ProDom; PD002129; Cofilin_ADF.1.
DR      SMART; SM00102; ADF.1.
DR      PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.
SQ      SEQUENCE 143 AA; 16510 MW; 408E0353DE61C05C CRC64;

Query Match          22.4%; Score 178; DB 10; Length 143;
Best Local Similarity 32.2%; Pred. No. 6,6e-09;
Matches 48; Conservative 32; Mismatches 53; Indels 16; Gaps

QY      4 ASGVSIADECIATFANDFRSGNKANKT-KETIFKIADNKRKEVIDEVSQ-EDDYEVFNSR 61
DB      5 ASGMAVHDDCKKFKLEL-----KAKRTYRFILTKIEKQKEVVEKLGEPSTSYEDFTG 59
QY      62 LEATKDSGNPNPARYAVDYEDVLCGEGSKSKYIFISVPSDPTLMSIYASTRENK 121
DB      60 LPADL-----CRAVYVDLDF-MTKENHOKSGRIFFIAMSPTARVRSKMIYASSKDRPK 111
QY      122 NALN-IHTSHADDKGDIEMKTVLAESG 149
DB      112 RELDGIQVELQATDPTMGLDVERSRAGG 140

RESULT 7
Q39250 PRELIMINARY: PRT: 139 AA.
ID      Q39250
AC      Q39250;
DT      01-NOV-1996 (TREMBlrel. 01, Created)
DT      01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT      01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE      ACTIN DEPOLYMERIZING FACTOR 1.
GN      ADF1 OR F16L2.220.
OS      Arabidopsis thaliana (Mouse-ear cress).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC      Eustrodiata II; Brassicales; Brassicaceae; Arabidopsis.
OX      NCBI_TaxID=3702;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=95148729; PubMed=7846151;
RA      Newman T., De Brulin F.J., Green P., Keegstra K., Kende H.,
RA      McIntosh T., Ohlrogge J., Raikhel N., Somerville S., Thomasnow M.,
RA      Retzel E., Somerville C.;
RT      "Genes galore: a summary of methods for accessing results from large-
RT      scale partial sequencing of anonymous Arabidopsis cDNA clones.";
RL      Plant Physiol. 106:1241-1255(1994).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      STRAIN=COLUMBIA;
RA      Staiger C.J., Ashworth S.L.;

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RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Dong C.H., Chua N.H.;  
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Jordan N., Bangert S., Wiedelmann R., Voss H., Unseid M., Mewes H.W.,  
 RA Rudd S., Lemcke K., Mayer K.F.X., Queller F., Salanoubat M.,  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA Arabidopsis sequencing project;  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U48938; AAB03696.1; -  
 DR EMBL: AF102173; AAC72407.1; -  
 DR EMBL: AL162459; CAB88325.1; -  
 DR HSSP: P37167; 1CNU.  
 DR Mendel: 34518; Arabid:1044;34518.  
 DR Mendel: 6289; Arabid:1044;6289.  
 DR InterPro: IPR002108; Cofilin\_ADF.  
 DR Pfam: PF00241; Cofilin\_ADF; 1.  
 DR ProDom: PD002129; Cofilin\_ADF; 1.  
 DR SMART: SM00102; ADF; 1.  
 DR PROSITE: PS00325; ACTIN\_DEPOLYMERIZING; 1.  
 DR SEQUENCE 139 AA; 16112 MW; E9429E0FE23A944F CRC64;

Query Match 22.2%; Score 177; DB 10; Length 139;  
 Best Local Similarity 32.4%; Pred. No. 7.8e-09;  
 Matches 45; Conservative 33; Mismatches 45; Indels 16; Gaps 6;

QY 4 ASGVSIADCTAFAFNDFRMSGNKANKT-KETIFKADNKKKEVVIDEVSQ-EDYEVFRSR 61  
 DB 5 ASGMVHDDCKLFLKLEL-----KAKRTHRIYVKKIEKQKQVVEVGPDIQYEEFAAC 59  
 QY 62 LEATKSKGNPAPRYAVYDEVYDGGEGKRSKIVISWPSDPTLMSMTASTRENK 121  
 DB 60 LPED-----CRYAVYDFD-VTAENCQSKRIFIAWCPDIKVRSMKYASSKDRK 111  
 QY 122 NALN-IHTSIHADKGDIE 139  
 DB 112 RELDGIQVELQATDPPEMD 130  
 RESULT 8  
 ID 09LO81 PRELIMINARY; PRT; 140 AA.  
 AC 09LO81;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE T1N6.16 PROTEIN.  
 GN T1N6.16.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC Eusticoidis II; Brassicales; Brassicaceae; Arabidopsids.  
 OC NCBI\_TaxID=3702;  
 RX STRAIN-CV. COLUMBIA;  
 RA Liu S., Chan A., Lee J., Lenz C., Pham P., Sakano H.,  
 RA Toriumi M., Chin C., Choi E., Chung M., Gonzalez A.,  
 RA Hong Y., Liu A., Vaysberg M., Altafi H., Brooks S., Buehler E.,  
 RA Chao O., Lam L., Conway A., Hansen N., Johnson-Hopson C., Khan S.,  
 RA Kim C., Lam B., Miranda M., Nguyen M., Palm C., Shin F.,  
 RA Southwick A., Davis R., Ecker J., Federspiel N., Theologis A.,  
 RA "The sequence of BAC T1N6 from Arabidopsis thaliana chromosome 1.";  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AC009273; AAF78408.1; -  
 DR InterPro: IPR002108; Cofilin\_ADF.  
 DR Pfam: PF00241; Cofilin\_ADF; 1.

DR PRINTS: PR00006; COFILIN.  
 DR ProDom: PD002129; Cofilin\_ADF; 1.  
 DR SMART: SM00102; ADF; 1.  
 DR PROSITE: PS00325; ACTIN\_DEPOLYMERIZING; 1.  
 DR SEQUENCE 140 AA; 16341 MW; B9845FE24B637859 CRC64;

Query Match 21.7%; Score 173; DB 10; Length 140;  
 Best Local Similarity 33.3%; Pred. No. 1.8e-08;  
 Matches 46; Conservative 28; Mismatches 48; Indels 16; Gaps 6;

QY 4 ASGVSIADCTAFAFNDFRMSGNKANKT-KETIFKADNKKKEVVIDEVSQ-EDYEVFRSR 62  
 DB 5 ASGMVHDDCKLFLKLEL-----KAKRTHRIYVKKIEKQKQVVEVGPDIQYEEFAAC 60  
 QY 63 LEATKSKGNPAPRYAVYDEVYDGGEG-KRSKIVISWPSDPTLMSMTASTRENK 121  
 DB 61 PEDE-----CRYAVYD-YDETPENCQSKRIFIAWCPDIKVRSMKYASSKDRK 111  
 QY 122 NALN-IHTSIHADKGDIE 138  
 DB 112 RELDGIQVELQATDPPEMD 129

RESULT 9  
 ID 09FV12 PRELIMINARY; PRT; 139 AA.  
 AC 09FV12;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE ACTIN-DEPOLYMERIZING FACTOR 1.  
 GN ADF1.  
 OS Petunia hybrida (Petunia).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; eusticoidis I; Solanales; Solanaceae; Petunia.  
 OC NCBI\_TaxID=4102;  
 RX STRAIN-CV. COLUMBIA;  
 RA Mun J.H., Yu H.J., Lee H.S., Kwon Y.M., Lee J.S., Lee I., Kim S.G.,  
 RT "Two closely related cDNAs encoding actin-depolymerizing factors of  
 RL petunia are mainly expressed in vegetative tissues."  
 RL Gene 257:167-176(2000).  
 DR EMBL: AF183903; AAG16973.1; -  
 DR InterPro: IPR002108; Cofilin\_ADF.  
 DR Pfam: PF00241; Cofilin\_ADF; 1.  
 DR ProDom: PD002129; Cofilin\_ADF; 1.  
 DR SMART: SM00102; ADF; 1.  
 DR PROSITE: PS00325; ACTIN\_DEPOLYMERIZING; 1.  
 DR SEQUENCE 139 AA; 16041 MW; 008073E2CA28F0B CRC64;

Query Match 21.5%; Score 171; DB 10; Length 139;  
 Best Local Similarity 29.7%; Pred. No. 2.8e-08;  
 Matches 44; Conservative 36; Mismatches 52; Indels 16; Gaps 6;

QY 4 ASGVSIADCTAFAFNDFRMSGNKANKT-KETIFKADNKKKEVVIDEVSQ-EDYEVFRSR 61  
 DB 5 ASGMVHDDCKLFLKLEL-----KAKRTHRIYVKKIEKQKQVVEVGPDIQYEEFAAC 59  
 QY 62 LEATKSKGNPAPRYAVYDEVYDGGEGKRSKIVISWPSDPTLMSMTASTRENK 121  
 DB 60 LPED-----CRYAVYDFD-VTAENCQSKRIFIAWCPDIKVRSMKYASSKDRK 111  
 QY 122 NALN-IHTSIHADKGDIEKTVLAAS 148  
 DB 112 RELDGIQVELQADPTEMLDVIOSRAN 139  
 RESULT 10  
 ID 041764



ID 041764 PRELIMINARY; PRT; 139 AA.  
 AC 041764;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE ACTIN DEPOLYMERIZING FACTOR.  
 GN ZMABp3.  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;  
 OC Panicoideae; Andropogoneae; Zea.  
 NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LEAF;  
 RA Lopez I., Anthony R.G., MacIver S.K., Jiong C.J., Khan S., Weeds A.G.,  
 RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(0).  
 DR EMBL; X97726; CAA66311.1; -.  
 DR HSSP; P37167; ICNU  
 DR Mendel; 11141; Zeama;1044;11141.  
 DR InterPro: IPR002108; Cofilin\_ADF.  
 DR Pfam: PF00241; Cofilin\_ADF; 1.  
 DR ProDom: PD002129; Cofilin\_ADF; 1.  
 DR SMART; SM00102; ADF; 1.  
 SQ SEQUENCE 139 AA; 15900 MW; 28FC82C518022C87 CRC64;

Query Match 21.4%; Score 170; DB 10; Length 139;  
 Best Local Similarity 30.9%; Pred. No. 3.4e-08;  
 Matches 42; Conservative 28; Mismatches 52; Indels 14; Gaps 5;

QY 5 GGVSIADCECTAENDFRMSGNKANKTKFTIKIDNKEVYIDEV-SQEEDEYFRRSLK 63  
 DB 6 SGVAVNDECMKFGELQ----SKRLHREITPKMDKEIYVDQVGDATSYDFTNSLP 61  
 QY 64 ATKDSGNPAPRYAVYDEVYDLGGEGKRSKIVFISWVPSDPTLMSIYASTRENLEKNA 123  
 DB 62 END-----CRYAIYDFDF-VTAEDVOKSKRIFFIILMSPSSAKAKYSKMLYASSNOKFNSG 113  
 QY 124 LN-IHTSIHADKGD 138  
 DB 114 LNGIQLVQLATDASEI 129

RESULT 11  
 Q9XEN2 PRELIMINARY; PRT; 138 AA.  
 ID Q9XEN2;  
 DT 01-NOV-1999 (TREMBlrel. 12, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE ACTIN DEPOLYMERIZING FACTOR (FRAGMENT).  
 OS Populus alba x Populus tremula.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Malpighiales; Salicaceae; Populus.  
 NCBI\_TaxID=80863;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=COLD ACCLIMATIZED BARK;  
 RA Coleman G.D.;  
 RT "Partial mRNA sequence of an actin depolymerizing factor from  
 RT Populus.";  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF112887; AAD3407.1; -.  
 DR HSSP; P37167; ICNU.  
 DR InterPro: IPR002108; Cofilin\_ADF.  
 DR Pfam: PF00241; Cofilin\_ADF; 1.  
 DR PRINTS; PR00006; COFILIN.  
 DR ProDom: PD002129; Cofilin\_ADF; 1.  
 DR SMART; SM00102; ADF; 1.  
 FT NON\_TER 1 1

SO SEQUENCE 138 AA; 15936 MW; 9B640D2FD497AA1F CRC64;

Query Match 21.2%; Score 169; DB 10; Length 138;  
 Best Local Similarity 29.9%; Pred. No. 4.2e-08;  
 Matches 44; Conservative 34; Mismatches 55; Indels 14; Gaps 5;

QY 4 ASGVSIADCECTAENDFRMSGNKANKTKFTIKIDNKEVYIDEV-SQEEDEYFRRSLK 62  
 DB 4 SSGMVAADHSKIAFVELQ----KKVHRYVIFKIDKKREKVEVTGGPASVEDFTASL 59;  
 QY 63 EATKDSGNPAPRYAVYDEVYDLGGEGKRSKIVFISWVPSDPTLMSIYASTRENLEKNA 122  
 DB 60 PEND-----CRYAVYDFDF-VTSENCQSKRIFFIILMSPSSAKAKYSKMLYASSNOKFNSG 111  
 QY 123 ALN-IHTSIHADKGDIEKTVLAAS 148  
 DB 112 ELDGIVHEIQATDPTMDLEVIERRAN 138

RESULT 12  
 Q9FEU7 PRELIMINARY; PRT; 139 AA.  
 ID Q9FEU7;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE ACTIN DEPOLYMERIZING FACTOR 4.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=COLUMBIA;  
 RX MEDLINE=99087489; PubMed=9872454;  
 RA Nakamura Y., Sato S., Asamizu E., Kaneko T., Kotani H., Miyajima N.,  
 RA Tabata S.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. VII.  
 RT Sequence features of the regions of 1,013,767 bp covered by sixteen  
 RT physically assigned P1 and TAC clones.";  
 RL DNA Res. 5:297-308(1998).  
 DR EMBL; AB015475; BAB08357.1; -.  
 DR InterPro: IPR002108; Cofilin\_ADF.  
 DR Pfam; PF00241; Cofilin\_ADF; 1.  
 DR PRINTS; PR00006; COFILIN.  
 DR ProDom; PD002129; Cofilin\_ADF; 1.  
 DR SMART; SM00102; ADF; 1.  
 DR PROSITE; PS00325; ACTIN DEPOLYMERIZING; 1.  
 SQ SEQUENCE 139 AA; 16034 MW; 57F95F557F42F863 CRC64;

Query Match 21.2%; Score 169; DB 10; Length 139;  
 Best Local Similarity 30.9%; Pred. No. 4.2e-08;  
 Matches 43; Conservative 34; Mismatches 46; Indels 16; Gaps 6;

QY 4 ASGVSIADCECTAENDFRMSGNKANKTKFTIKIDNKEVYIDEV-SQEEDEYFRRSLK 61  
 DB 5 ASGMVAVHDDCKRLEL-----KAKRTHRFIVYKTEEKOKOYIVAEVEPTLYEDFAAS 59  
 QY 62 LEATKDSGNPAPRYAVYDEVYDLGGEGKRSKIVFISWVPSDPTLMSIYASTRENLEKNA 121  
 DB 60 LPADL-----CRYAIYDFDF-VTAENCOQSKRIFFIILMSPSSAKAKYSKMLYASSNOKFNSG 111  
 QY 122 NALN-IHTSIHADKGDIE 139  
 DB 112 RELDGIQLVQLATDPTEND 130

RESULT 13  
 Q9ZSK3 PRELIMINARY; PRT; 139 AA.  
 ID Q9ZSK3

AC 09ZSK3;  
 DT 01-MAY-1999 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)  
 DE ACTIN DEPOLYMERIZING FACTOR 4.  
 GN ADF4.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Dong C.H., Chua N.H.;  
 RT "Arabidopsis Actin Depolymerizing Factor 4.\*";  
 RL Submitted (Oct-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF102822; AAD09110.1; -.  
 DR HSSP: P37167; 1CNU.  
 DR Mendel: 36497; Arabid.1044;36497.  
 DR InterPro: IPR002108; Cofilin\_ADF.  
 DR Pfam: PF00241; cofilin\_ADF.1.  
 DR ProDom: PD002129; Cofilin\_ADF.1.  
 DR SMART: SM00102; ADF.1.  
 DR PROSITE: PS00325; ACTIN DEPOLYMERIZING.1.  
 SQ SEQUENCE 139 AA; 16150 MW; 4CF95F557F56962 CRC64;

Query Match 21.0%; Score 167.5; DB 10; Length 139;  
 Best Local Similarity 30.3%; Pred. No. 5.8e-08;

Matches 44; Conservative 35; Mismatches 47; Indels 19; Gaps 7;

OY 4 ASGVSTADECTIAFNDFRMSGNKANKT-KFIFKIDNKKKEVIDEVSQ-EEDYEFRRSR 61  
 DB 5 ASGVAVHDDCKLFLEL-----KAKRTHRYVYKIEKQKOVIVEKGEPIITLTFEFAAS 59  
 OY 62 LEATKSKGNPAPRYAVYDVEYDLGGEGKRSKIVTISWPSPTPLMSIYASTRENK 121  
 DB 60 LPADL-----CRAVAYDFDF-VTAENCQSKIFFIAMCPVAKYRSKMYASSKDRRK 111  
 OY 122 NALN-IHTSIHADKGDIE---WKT 142  
 DB 112 RELDGRQVELQATDPTPEMDLDWKS 136  
 RESULT 14  
 ID 043694 PRELIMINARY; PRT; 139 AA.  
 AC 043694;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)  
 DE ACTIN DEPOLYMERIZING FACTOR.  
 GN ZMABP2.  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;  
 OC Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN-CV. A188; TISSUE-POLLEN;  
 RA Lopez I., Anthony R.G., Maciver S.K., Jiong C.J., Khan S., Weeds A.G.,  
 RA Hussey P.J.;  
 RL EMBL: X97725; CA66310.1; -.  
 DR HSSP: P37167; 1CNU.  
 DR Mendel: 11142; Zeama.1044;11142.  
 DR InterPro: IPR002108; Cofilin\_ADF.  
 DR Pfam: PF00241; cofilin\_ADF.1.  
 DR ProDom: PD002129; Cofilin\_ADF.1.  
 DR SMART: SM00102; ADF.1.  
 DR PROSITE: PS00325; ACTIN DEPOLYMERIZING.1.  
 SQ SEQUENCE 139 AA; 16083 MW; F96A48B00F658604 CRC64;

Query Match 20.6%; Score 164; DB 10; Length 139;  
 Best Local Similarity 30.4%; Pred. No. 1.2e-07;  
 Matches 42; Conservative 30; Mismatches 50; Indels 16; Gaps 6;

OY 4 ASGVSTADECTIAFNDFRMSGNKANKT-KFIFKIDNKKKEVIDEVSQ-EEDYEFRRSR 61  
 DB 5 SGLVAVDECKYKFRDL-----KARRSFYVIRIDCKMEIKVDRLGEPCNGQGDFTDS 59  
 OY 62 LEATKSKGNPAPRYAVYDVEYDLGGEGKRSKIVTISWPSPTPLMSIYASTRENK 121  
 DB 60 LPADL-----CRAVAYDFDF-VENCQSKIFFEWSPTARTSRKMYASSKDRFR 111  
 OY 122 NALN-IHTSIHADKGDID 138  
 DB 112 RELDGIQCEIQATDPSEM 129

RESULT 15

ID 09ZSK2 PRELIMINARY; PRT; 146 AA.

AC 09ZSK2;  
 DT 01-MAY-1999 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)  
 DE ACTIN DEPOLYMERIZING FACTOR 6.

OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Dong C.H., Chua N.H.;  
 RT "Arabidopsis Actin Depolymerizing Factor 6.\*";  
 RL Submitted (Oct-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF102824; AAD09112.1; -.  
 DR EMBL: AF183576; AAF01035.1; -.  
 DR HSSP: 003048; 1COF.  
 DR Mendel: 36499; Arabid.1044;36499.  
 DR InterPro: IPR002108; Cofilin\_ADF.  
 DR Pfam: PF00241; cofilin\_ADF.1.  
 DR PRINTS: PR00006; COFILIN.  
 DR ProDom: PD002129; Cofilin\_ADF.1.  
 DR SMART: SM00102; ADF.1.  
 SQ SEQUENCE 146 AA; 16708 MW; A97CEF5D2CC17A85 CRC64;

Query Match 20.4%; Score 162; DB 10; Length 146;  
 Best Local Similarity 28.1%; Pred. No. 2e-07;  
 Matches 41; Conservative 38; Mismatches 53; Indels 14; Gaps 5;

OY 5 SGVSTADECTIAFNDFRMSGNKANKT-KFIFKIDNKKKEVIDEVSQ-EEDYEFRRSR 63  
 DB 13 SGMVAVDECKTFLLEQ-----RKTHRYVYFKIDSKKEVVEKGTGNPTSEYDDFLASLP 68  
 OY 64 ATKDSKGNPAPRYAVYDVEYDLGGEGKRSKIVTISWPSPTPLMSIYASTRENK 123  
 DB 69 -----DMDCRVAVYDFDF-VTSENCKSKIFFEAWSPSTGIRAKVLYSTRSKQLSRE 120  
 OY 124 L-NHTSIHADKGDIEKTVLAAS 148  
 DB 121 LOGIHYEIQATDPTPEVDLEVERAN 146

RESULT 16  
 ID 09ZSK4

ID Q9ZSK4 PRELIMINARY; PRT; 139 AA.  
AC Q9ZSK4;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE ACTIN DEPOLYMERIZING FACTOR 3 (PUTATIVE ACTIN DEPOLYMERIZING FACTOR 3 PROTEIN).  
DE ADF3 OR MN10.12.  
GN Arabidopsis thaliana (Mouse-ear cress).  
OS Arabidopsis thaliana; Streptophyta; Embryophyta; Tracheophyta;  
OC Eukaryota; Viridiplantae; Streptophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.  
OC NCBI\_TaxID=3702;  
OX  
RN  
RP SEQUENCE FROM N.A.  
RT "Arabidopsis Actin Depolymerizing Factor 3."  
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
RN  
RP SEQUENCE FROM N.A.  
RT Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
RN  
RP SEQUENCE FROM N.A.  
RT Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
RN  
RP STRAIN=COLUMBIA;  
RC MEDLINE=99087489; PubMed=9872454;  
RX Nakamura Y., Sato S., Asamizu E., Kaneko T., Kotani H., Miyajima N., Tabata S.;  
RA "Structural analysis of Arabidopsis thaliana chromosome 5. VII. Sequence features of the regions of 1,013,767 bp covered by sixteen physically assigned P1 and TAC clones."  
RT DNA Res. 5:297-308(1998).  
RL  
RN  
RP SEQUENCE FROM N.A.  
RT  
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L., Canfield P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kaniwa A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;  
RA "Full length cDNA of gene MN10.12 (GI:9757909)."  
RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
RL  
DR EMBL; AF102821; AAD09109.1;  
DR EMBL; AB015475; BAB08356.1;  
DR EMBL; AF360169; AAK25879.1;  
DR HSSP; P37167; ICNU.  
DR Mendel; 36496; Arah:1044;36496.  
DR InterPro: IPR002108; Cofilin\_ADF.  
DR Pfam; PF00241; Cofilin\_ADF.1.  
DR ProDom; PD002129; Cofilin\_ADF.1.  
DR SMART; SM00102; ADF.1.  
DR PROSITE; PS00325; ACTIN\_DEPOLYMERIZING; 1.  
SQ SEQUENCE 139 AA; 15922 MW; D3325AA71D0D102E CRC64;

Query Match 19.8%; Score 158; DB 10; Length 139;  
Best Local Similarity 29.3%; Pred. No. 4.3e-07;  
Matches 41; Conservative 35; Mismatches 46; Indels 18; Gaps 7;

QY 4 ASGVSIADECTAFAFNDPFRSGNKNANKT-KTIFIKADNKKVEYVDEV-SQEDYEYFVSRL 61  
DB 5 ASGVAHDVCDKFKLMEI-----KTKRTHRFITIKTEELQKQYIKVEIPGQTHDLAAS 59  
QY 62 LEATGDSKGNPAPRAYVDEYDGGEGG-KRSKIVFISWPSDPTLMSMISTASTREN 120  
DB 60 LPAD-----CRAIYD--FDYSSGCVPRSRILEFVAMSPDTRAKVSKMITYASSKDRF 110  
QY 121 KNALN-IHTSIHADKGDIE 139  
DB 111 KRELDSIGVELQATDPTEMD 130  
RESULT 17  
Q9M594 PRELIMINARY; PRT; 140 AA.  
AC Q9M594;

DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE ACTIN DEPOLYMERIZING FACTOR.  
DE Elaeis guineensis var. tenera (Oil palm).  
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Arecaceae; Elaeis.  
OC NCBI\_TaxID=51953;  
OX  
RN  
RP SEQUENCE FROM N.A.  
RC TISSUE=MESOCARP;  
RA Cha T.S., Shah F.H.;  
RT "Elaeis guineensis var. Tenera actin depolymerizing factor cDNA clone."  
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF236068; AAF60173.1;  
DR InterPro: IPR002108; Cofilin\_ADF.  
DR Pfam; PF00241; Cofilin\_ADF.1.  
DR ProDom; PD002129; Cofilin\_ADF.1.  
DR SMART; SM00102; ADF.1.  
SQ SEQUENCE 140 AA; 16199 MW; 9FA2AE19785A7935 CRC64;

Query Match 19.8%; Score 158; DB 10; Length 140;  
Best Local Similarity 28.4%; Pred. No. 4.3e-07;  
Matches 42; Conservative 36; Mismatches 56; Indels 14; Gaps 5;

QY 5 SGVSIADCEITAFNDFRSGNKNANKT-KTIFIKADNKKVEYVDEV-SQEDYEYFVSRL 63  
DB 4 SGMVAADSKSTFLELK-----RKHYRYVIFMIDKKKEVEYKGTGPESTDDTALP 59  
QY 64 ARKDSKGNPAPRAYVDEYDGGEGG-KRSKIVFISWPSDPTLMSMISTASTREN 123  
DB 60 VND-----CRAIYDDE--VTEONCKSKIFLISMSVSRSKMLATSKDRFRHE 111  
QY 124 IN-IHTSIHADKGDIEKTVLAESGG 150  
DB 112 LDGVHVEIQATDPTEMDLEVLDRAKLG 139

RESULT 18  
Q9AY76 PRELIMINARY; PRT; 145 AA.  
AC Q9AY76;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE PUTATIVE ACTIN-DEPOLYMERIZING FACTOR.  
DE Oryza sativa (Rice).  
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Euphorbiaceae; Oryzaeae; Oryza.  
OC NCBI\_TaxID=4530;  
OX  
RN  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. NIPONBARE;  
RA Buell C.R., Yuan Q., Moffet K.S., Hill J.N., Burr P.C., Hsiao J., Zisman V., Pal G., Bowman C.L., Fujii C.Y., Vanaken S.E., Bowman C.L., Craven B., Utterback T.R., Khalek H., Feldblyum T.V., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;  
RA "Oryza sativa chromosome 3 BAC OSJNBa0091319 genomic sequence."  
RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AC084320; AAK09235.1;  
SQ SEQUENCE 145 AA; 16794 MW; 7C853B09D3B3B110 CRC64;

Query Match 19.6%; Score 156; DB 10; Length 145;  
Best Local Similarity 26.7%; Pred. No. 6.9e-07;  
Matches 39; Conservative 39; Mismatches 54; Indels 14; Gaps 5;  
QY 4 ASGVSIADECTAFAFNDPFRSGNKNANKT-KTIFIKADNKKVEYVDEV-SQEDYEYFVSRL 62  
DB 11 SGMVAADIRTFLELMK-----KAPRYVIFKIEKQKQYVVEKGTATTESYDDFLAST 66

OS Arabidopsis thaliana (Mouse-ear cress).  
 OS Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 CC eucosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OK NCBI\_taxonomy:3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV, COLUMBIA;  
 RX MEDLINE=20083487; PubMed=10617197;  
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-T., Town C.D.,  
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldbaum T.V.,  
 RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,  
 RA Cronin L.A., Shera M., Vankken S.E., Umeyam L., Tallon L.J., Gill J.E.,  
 RA Adams M.D., Carreira A.J., Cressy T.H., Goodman H.M., Somerville C.R.,  
 RA Copenhagen G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,  
 RA Salzberg S.L., Fraser C.M., Venter J.C.;  
 RT "Sequence and analysis of chromosome II of Arabidopsis thaliana";  
 RL Nature 402:761-768(1999).  
 DR EMBL; AC006593; AAD2065.1; -.  
 DR HSSP; Q03048; ICOF.  
 DR InterPro; IPR002108; Cofilin\_ADF.  
 DR Pfam; PF00241; cofilin\_ADF.1.  
 DR PRINTS; PR00006; COFILIN.  
 DR PRODOM; PD002129; Cofilin\_ADF.1.  
 DR SMART; SM00102; ADF.1.  
 SQ SEQUENCE 132 AA; 15233 MW; 70A194270CB55933 CRC64;  
 Query Match 19.1%; Score 152; DB 10; Length 132;  
 Best Local Similarity 27.1%; Pred. No. 1,4e-06;  
 Matches 39; Conservative 38; Mismatches 53; Indels 14; Gaps 5;  
 QY 7 VSADECITAFNDFRMSGNKANKTKFIIFKTDANKREYVIDEV-SQEDYEVSRLSAT 65  
 Db 1 MGVADESKTFTLEIQ---RKTHRYVVEFKIDESKEVEVEKGNPTESYDFTLSLP-- 54  
 QY 66 KDSKGNPAPRAVAVDYEDLDGGEGKRSKIYFISVPSDFPLMSIYASTRENKML- 124  
 Db 55 -----DNDCRVAVIDFD-VTSENCQKSKIFPFAMSPSTSGIRAKVILKSTKQDLSREL 108  
 QY 125 NIHTSIHADKGDIEEMKVTILAEAS 148  
 Db 109 GIHWEIFQATDPTFVDLFEVLRERAN 132  
 RESULT 21  
 ID Q39251 PRELIMINARY; PRT; 137 AA.  
 AC Q39251;  
 DT 01-NOV-1996 (TREMblrel. 01, created)  
 DT 01-NOV-1996 (TREMblrel. 01, last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, last annotation update)  
 DE ACTIN DEPOLYMERIZING FACTOR 2.  
 GN ADF2.  
 OC Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 CC eucosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OK NCBI\_taxonomy:3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=COLUMBIA;  
 RX MEDLINE=95148729; PubMed=7846151;  
 RA Newman T., De Bruijn F.J., Green P., Keegstra K., Kende H.,  
 RA McIntosh L., Ohlrogge J., Raikhel N., Somerville S., Thomasnow M.,  
 RA Retzel E., Somerville C.;  
 RT "Genes galore: a summary of methods for accessing results from large-  
 scale partial sequencing of anonymous Arabidopsis cDNA clones.";  
 RL Plant Physiol. 106:1241-1255(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=COLUMBIA;  
 RX Stalger C.J., Ashworth S.L.;

RL Submitted (FEB-1996) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: U48939; AAB03697.1; -  
 DR HSSP: P37167; ICNU.  
 DR InterPro: IPR002108; Cofilin\_ADF.  
 DR Pfam: PF00241; Cofilin\_ADF.1.  
 DR ProDom: PD002129; Cofilin\_ADF.1.  
 DR SMART: SM00102; ADF.1.  
 DR PROSITE: PS00325; ACTIN DEPOLYMERIZING; 1.  
 SQ SEQUENCE 137 AA; 15745 MW; BE28852817394046 CRC64;

Query Match 19.1%; Score 152; DB 10; Length 137;  
 Best Local Similarity 30.6%; Pred. No. 1.5e-06;  
 Matches 41; Conservative 31; Mismatches 44; Indels 18; Gaps 7;

OY 4 ASGVSIADCTAIFNDFRSGNKANKT-KETLEKIDNKEVVIDEVSQ-EDDYEVFSR 61  
 DB 5 ASGVAHDDCKLKFEMEL-----KAKRTFRTIYKIED--KQIVYKLGEPESQSYDFAAS 57  
 OY 62 LEATKDSKGNAPRAYVDVEYDLGGGEGKRSKIVFISWSDPTLMSMTASTRENILK 121  
 DB 58 LPAD-----CRCTYDFDF-VTAENCQSKLFFIAMSPTAKVRKDMITAYSSKDRPK 109  
 OY 122 NALN-IHTSIHADD 134  
 DB 110 REDGIGYELQATD 123

RESULT 22  
 O9FHC4 PRELIMINARY; PRT: 130 AA.  
 AC O9FHC4; DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE ACTIN DEPOLYMERIZING FACTOR-LIKE.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OC NCBI\_Taxid=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=COLUMBIA;  
 RX MEDLINE=20181125; PubMed=10718197;  
 RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,  
 RA Tabata S.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence  
 RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC  
 RT clones."  
 RL DNA Res. 7:31-63(2000).  
 DR EMBL: AB019226; BAB10533.1; -  
 DR InterPro: IPR002108; Cofilin\_ADF.  
 DR Pfam: PF00241; Cofilin\_ADF.1.  
 DR PRINTS: PR00006; Cofilin.  
 DR ProDom: PD002129; Cofilin\_ADF.1.  
 DR SMART: SM00102; ADF.1.  
 DR PROSITE: PS00325; ACTIN DEPOLYMERIZING; 1.  
 SQ SEQUENCE 130 AA; 15281 MW; 23DE681D1081B430 CRC64;

Query Match 19.0%; Score 151; DB 10; Length 130;  
 Best Local Similarity 29.2%; Pred. No. 1.7e-06;  
 Matches 42; Conservative 34; Mismatches 50; Indels 18; Gaps 7;

OY 7 VSINDECTAANDFRSGNKANKT-KETLEKIDNKEVVIDEVSQ-EDDYEVFSRLEAT 65  
 DB 1 MAVDEEKLKLELAKRN---YREIFRI--DQOVVERKSPDNVDFNYLPN 54  
 OY 66 KDSKGNPAPRAYVDVEYDLGGGEGKRSKIVFISWSDPTLMSMTASTRENILK 124  
 DB 55 E-----CRAAYVD--FDFTTAENIGKSKLFFIAMSPTAKVRKDMITAYSSKDRPK 105

OY 125 N-IHTSIHADKGDIEKMTVLAE 147  
 DB 106 DGIYELQATDPSKMSLDIKSRA 129

RESULT 23  
 O9UAT4 PRELIMINARY; PRT: 293 AA.  
 ID O9UAT4; DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE CONTAINS SIMILARITY TO C. ELEGANS ACTIN DEPOLYMERIZING FACTOR UNC-60  
 DE (SP:007750).  
 GN UNC-60.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Pelodierinae; Caenorhabditis.  
 OC NCBI\_Taxid=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RX MEDLINE=94150718; PubMed=7906398;  
 RA Wilson R., Alnsough R., Anderson K., Baynes C., Berks M.,  
 RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,  
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,  
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,  
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,  
 RA Lightning J., Lloyd C., McMuray A., Mortimore B., O'Callaghan M.,  
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,  
 RA Smaildon N., Smith A., Sonnenhammer E., Staden R., Sulston J.,  
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,  
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Woldman P.;  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 RT elegans."  
 RL Nature 368:32-38(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RA Courtney L., Bauer C., Woldman P.;  
 RT "The sequence of C. elegans cosmid F53E2."  
 RL Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RA Waterston R.;  
 RL Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF125953; AAD14704.1; -  
 DR HSSP: P37167; ICNU.  
 DR InterPro: IPR002108; Cofilin\_ADF.  
 DR Pfam: PF00241; Cofilin\_ADF.2.  
 DR ProDom: PD002129; Cofilin\_ADF.2.  
 DR SMART: SM00102; ADF.1.  
 DR PROSITE: PS00325; ACTIN DEPOLYMERIZING; 2.  
 SQ SEQUENCE 293 AA; 32636 MW; 1C18733BA45B6400 CRC64;

Query Match 18.9%; Score 150.5; DB 5; Length 293;  
 Best Local Similarity 28.6%; Pred. No. 5.3e-06;  
 Matches 44; Conservative 35; Mismatches 54; Indels 21; Gaps 7;

OY 4 ASGVSIADCTAIFNDFRSGNKANKT-KETLEKIDNKEVVIDEVSQ-EDDYEVFSR 61  
 DB 143 ASGVAVDSDCKNAAD---LLHNK-HQHSYIFKIDNDAIYVERGKRNAPYAEFVEEM 198  
 OY 59 RSRLATKDSKGNAPRAYVDVEYDL--GGGEGKR--SKIYFISWSDPTLMSMTASTRENILK 114  
 DB 199 KLVLEDGEGEC-----RRAANDVEYTVOROGAEGSTLTKLVYVYCPDNAPVRRRLA 252  
 OY 115 STRENILKALNINHT--SIHADKGDIEKMTVLAE 146  
 DB 253 SSVRLKASLIGLESIFVOYASSEMSDLDEKSVSKD 286

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RESULT 24
ID 065603 PRELIMINARY; PRT; 130 AA.
AC 065603;
DT 01-AUG-1998 (TREMblrel. 07, Created)
DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE ACTIN DEPOLYMERIZING FACTOR - LIKE PROTEIN (ACTIN DEPOLYMERIZING
DE FACTOR-LIKE PROTEIN).
GN M7J2.40 OR AT4G25390.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Barques M., Perez-Perez A., Terol J., Torres A.,
RA Perez-Alonso M., Hohelsel J., Mewes H.W., Mayer K., Schueller C.,
RN Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RA Barques M., Perez-Perez A., Terol J., Torres A., Perez-Alonso M.,
RA Mewes H.W., Lemcke K., Mayer K.F.X.;
RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL022197; CA18167.1; -
DR EMBL; AL161563; CAB81369.1; -
DR HSSP; P37167; 1CND.
DR Mendel; 29815; Arath;1044;29815.
DR InterPro: IPR002108; Cofilin_ADF.
DR Pfam; PF00241; Cofilin_ADF; 1.
DR ProDom; PD002129; Cofilin_ADF; 1.
DR SMART; SM00102; ADF; 1.
DR PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.
SQ SEQUENCE 130 AA; 15217 MW; 8BCB94D274897F2 CRC64;

Query Match 18.8%; Score 150; DB 10; Length 130;
Best Local Similarity 27.3%; Pred. No. 2.1e-06;
Matches 39; Conservative 38; Mismatches 50; Indels 16; Gaps 6;

QY 7 VSTADCEITAFNDFRMSGNANKTKFIETKIANKKEVIVDEY-SQEDIEVFRSRLEAT 65
DB 1 MAVEDECKLFLFKLSKRN---YRFTIFRI--DGOQVVEKLGNDPEYDDEFTASIPAN 54
QY 66 KDKSGNPAPRAYVDEYDLGGEGKRSKIIVFTSWPDSPTPLMSMTASTRENKMAIN 125
DB 55 E-----CRYAVFDDE-ITDENCQKSKFTFTAMSPDSSRYMKMYASSKDRFRELD 106

QY 126 -IHTSIHADKGDIEKTVLAEA 147
DB 107 GIOVELQATPDSSEMSFDIIRSA 129

RESULT 25
ID 09R0P5 PRELIMINARY; PRT; 165 AA.
AC 09R0P5;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE SID3P.
GN DSN OR SID23.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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RN [1]
RP SEQUENCE FROM N.A.
RA Seki N., Hattori A., Hayashi A., Kozuma S., Muramatsu M., Saito T.;
RT "Mouse actin depolymerizing factor sid3p."
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB025406; BAA84691.1; -
DR HSSP; P18282; 1AK6.
DR MGD; MGI:1929270; Dsn.
DR InterPro: IPR002108; Cofilin_ADF.
DR Pfam; PF00241; Cofilin_ADF; 1.
DR PRINTS; PR00006; COFILIN.
DR ProDom; PD002129; Cofilin_ADF; 1.
DR SMART; SM00102; ADF; 1.
DR PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.
SQ SEQUENCE 165 AA; 18521 MW; 42BD07984C9B3667 CRC64;

Query Match 18.8%; Score 150; DB 11; Length 165;
Best Local Similarity 27.4%; Pred. No. 2.9e-06;
Matches 46; Conservative 29; Mismatches 59; Indels 34; Gaps 7;

QY 3 LASGVSIADECITAFNDFRMSGNKA-----NKKFTIFKIANKKEVIVDEVSQEDIEY 57
DB 1 MASGVQYADVCHRFYDMKVKCSTPEIKRKRAVFLCSADKKCIYV-----EGSKET 55
QY 58 FRSRLSAT-----KDSKGNPAPRAYVDEYDLGGEGKRSKIYFISWPS 103
DB 56 LVGDVGATITDPKHFYGMLEKDC-----RYALDASFET--KESRKELMFLMAPE 107

QY 104 DPTPLMSMTASTRENKMAIN-IHTSIHADKGDIEKTVLAESG 150
DB 108 QAPLRSKMIYASSKDAIKKFKPGIKHEYQANGPEDLN-RTCIAEKELGG 154

RESULT 26
ID 09ZNT3 PRELIMINARY; PRT; 143 AA.
AC 09ZNT3;
DT 01-MAY-1999 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE ACTIN DEPOLYMERIZING FACTOR 5.
GN ADF5.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Dong C.H., Chua N.H.;
RT "Arabidopsis Actin Depolymerizing Factor 5."
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Totiumi M., Yu G., Bowser L.,
RA Carlinch P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full length cDNA of gene T24121.11/At2g16700 (GI:4581113).";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF102825; AAD09113.1; -
DR EMBL; AF102823; AAD09111.1; -
DR EMBL; AF360302; AAK26012.1; -
DR HSSP; P37167; 1CND.
DR Mendel; 36498; Arath;1044;36498.
DR Mendel; 36500; Arath;1044;36500.
DR InterPro: IPR002108; Cofilin_ADF.
DR Pfam; PF00241; Cofilin_ADF; 1.
DR ProDom; PD002129; Cofilin_ADF; 1.

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DR SMART; SM00102; ADF; 1.  
SQ SEQUENCE 143 AA; 16468 MW; 570BF0222BE043CA CRC64;

Query Match 18.8%; Score 149.5; DB 10; Length 143;  
Best Local Similarity 29.8%; Pred. No. 2.7e-06;  
Matches 42; Conservative 32; Mismatches 48; Indels 19; Gaps 7;

QY 1 MALA-----SGVSTADECTAFNDFRMSGNKANKTKFTIFFIADNKKREVIDEV-SQEDD 54  
DB 1 MAMAFKMATFTGMRVDECTSSFMD--MKMKRVH--RYIVFKIEKSRKYVTVDKVGAGES 56  
QY 55 YEVRFSRLKATKDSKGNAPRAYVYDEVYDGGGSKRSKIYFISWSPDPTLMSIYA 114  
DB 57 Y-----HDEEDSLPVDCRYAVFDFDF-VTVNCRKSKIFFIAMSPKAKIILYA 108  
QY 115 STRENKKNAL-NHTSIHAD 134  
DB 109 TSKDGLRVRLEGIHVELQATD 129

RESULT 27  
Q9SM69  
ID Q9SM69 PRELIMINARY; PRT; 129 AA.  
AC Q9SM69  
DT 01-MAY-2000 (TRENBLREL. 13, Created)  
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)  
DT 01-JUN-2001 (TRENBLREL. 17, Last annotation update)  
DE PUTATIVE ACTIN DEPOLYMERIZING FACTOR.  
GN ADF.  
OS Malus domestica (Apple) (Malus sylvestris).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Rosales; Rosaceae; Malus.  
OX NCBI\_TaxID=3750;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. FLORINA; TISSUE=LEAVES INFECTED WITH VENTURIA INAEQUALIS;  
RA Rebl S., Rigatti R., Komjanc M.;  
RT "Cloning of an apple gene encoding actin depolymerizing factor  
RT (ADF).";  
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF179295; AAD51856.1; -  
DR HSSP; P37167; ICNU.  
DR InterPro; IPR002108; Cofilin\_ADF.  
DR Pfam; PF00241; Cofilin\_ADF.1.  
DR ProDom; PD002129; Cofilin\_ADF.1.  
DR SMART; SM00102; ADF; 1.  
DR PROSITE; PS00325; ACTIN\_DEPOLYMERIZING; 1.  
SQ SEQUENCE 129 AA; 15101 MW; DE09EFAFF511CD3 CRC64;

Query Match 18.7%; Score 148.5; DB 10; Length 129;  
Best Local Similarity 31.0%; Pred. No. 2.9e-06;  
Matches 39; Conservative 27; Mismatches 49; Indels 11; Gaps 5;

QY 26 KANKT-KFIIFKIDNKKVEVIDEVSQ-EEDYEVFRSLKATKSKGNAPRAYVYDEV 83  
DB 12 KAKRTYRIVYKIDKNEVIEKGEPAESYEDFTANLPNE-----CRYAYDFDF 64  
QY 84 DLGGGGRSKRIVFTSWSPDPTLMSIYASTRENKKNAL-NHTSIHADDKGIEKKT 142  
DB 65 -VYVENCHKSRIFVGVSPDPTARVRNKKMTIYASSKDRFKRELIDGLOVELQATDPSEIGADV 123

QY 143 VLAEAS 148  
DB 124 IKSRAN 129  
RESULT 28  
ID 065277 PRELIMINARY; PRT; 133 AA.  
AC 065277;

DT 01-AUG-1998 (TRENBLREL. 07, Created)  
DT 01-AUG-1998 (TRENBLREL. 07, Last sequence update)  
DT 01-JUN-2001 (TRENBLREL. 17, Last annotation update)  
DE F6N23.12 PROTEIN (PUTATIVE ACTIN-DEPOLYMERIZING FACTOR).  
GN F6N23.12 OR AT4G00680.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. COLUMBIA;  
RA WASHU;  
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. COLUMBIA;  
RA Geisel C.;  
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. COLUMBIA;  
RA Waterston R.;  
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Lamar B., Stoneking T., Stumpf J., Mewes H.W., Lemcke K.,  
RA Mayer K.F.X.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RC EU Arabidopsis sequencing project;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF058919; AAC13618.1; -  
DR EMBL; AL161472; CAB80877.1; -  
DR HSSP; P37167; ICNU.  
DR Mendel; 29660; Arabid.1044;29660.  
DR InterPro; IPR002108; Cofilin\_ADF.  
DR Pfam; PF00241; Cofilin\_ADF.1.  
DR ProDom; PD002129; Cofilin\_ADF.1.  
DR SMART; SM00102; ADF; 1.  
DR PROSITE; PS00325; ACTIN\_DEPOLYMERIZING; 1.  
SQ SEQUENCE 133 AA; 15659 MW; DDE45681C578912E CRC64;

Query Match 18.2%; Score 145; DB 10; Length 133;  
Best Local Similarity 30.1%; Pred. No. 6.3e-06;  
Matches 40; Conservative 29; Mismatches 48; Indels 16; Gaps 6;

QY 9 IADECTAFNDFRMSGNKANKT-KFIIFKIDNKKVEVIDEV-SQEDYEVFRSLKATK 66  
DB 3 VNDECKIFLEL-----KAKRTYRIVYKIDKAKAOVOIEKIGNEPEYDDFTSSIP--- 54  
QY 67 DSKGNAPRAYVYDEVYDGGGGRSKRIVFTSWSPDPTLMSIYASTRENKKNAL-N 125  
DB 55 ----DDECRIVAYDDFTT-EDNCOKSKIFFIAMSPDPTSRVSKMLYASSKDRFKREMEG 109  
QY 126 IHTSIHADDKGDI 138  
DB 110 IQVELQATDPSEM 122

RESULT 29  
Q9LZT3  
ID Q9LZT3 PRELIMINARY; PRT; 133 AA.  
AC Q9LZT3;  
DT 01-OCT-2000 (TRENBLREL. 15, Created)  
DT 01-OCT-2000 (TRENBLREL. 15, Last sequence update)  
DT 01-JUN-2001 (TRENBLREL. 17, Last annotation update)  
DE ACTIN DEPOLYMERIZING LIKE PROTEIN.  
GN F16L2.200.  
OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Jordan N., Bangerter S., Wiedelmann R., Voss H., Unseld M., Mewes H.W.,  
 RA Rudd S., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.,  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project;  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL162459; CAB82823.1; -;  
 DR InterPro; IPR002108; Cofilin\_ADF.  
 DR Pfam; PF00241; cofilin\_ADF; 1.  
 DR PRINTS; PR00006; COFILIN.  
 DR PRODOM; PD002129; Cofilin\_ADF; 1.  
 DR SMART; SM00102; ADF; 1.  
 SQ SEQUENCE 133 AA; 15904 MW; 26EFC58B62FE3C52 CRC64;

Query Match 18.2%; Score 144.5; DB 10; Length 133;  
 Best Local Similarity 31.4%; Pred. No. 7e-06;  
 Matches 43; Conservative 23; Mismatches 44; Indels 27; Gaps 7;

OY 11 DECTAFNDRMSGNKANKT-KFLIFKADNKKKEVIDE-----VSQEDYEVRSL 62  
 DB 5 DDCKLTFLEL-----KRRFRSTIVYKIEDN-MQVIEKHKKMGGERDSTEEFANSL 58  
 OY 63 EATKDSKGNPAPRYAVDVEYDLGGEGKRSKIYFISWVSDPTLTSMIYASTRENLN 122  
 DB 59 PADE-----CRAITDIEFVG-----ERKICFIAMSPSTAKMRKKMYSSKDKRFR 106  
 OY 123 ALN-IHTSHADDKGDI 138  
 DB 107 ELDGIGVEFHATDLTDI 123

RESULT 30  
 ID 015902 PRELIMINARY; PRT; 118 AA.  
 AC 015902;  
 DT 01-JAN-1998 (TREMblrel. 05, Created)  
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE ACTIN DEPOLYMERIZING FACTOR.  
 OS Toxoplasma gondii.  
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;  
 OC Toxoplasma.  
 OX NCBI\_TaxID=5811;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-RH;  
 RX MEDLINE-97418790; Pubmed-9274866;  
 RA Allen M.L., Dobrowolski J.M., Muller H., Sibley L.D., Mansour T.E.,  
 RT Cloning and characterization of actin depolymerizing factor from  
 RT Toxoplasma gondii.  
 RL Mol. Biochem. Parasitol. 88:43-52(1997).  
 DR EMBL; U62146; AAC47717.1; -;  
 DR HSSP; P37167; ICNU.  
 DR InterPro; IPR002108; Cofilin\_ADF.  
 DR Pfam; PF00241; cofilin\_ADF; 1.  
 DR PRODOM; PD002129; Cofilin\_ADF; 1.  
 DR SMART; SM00102; ADF; 1.  
 SQ SEQUENCE 118 AA; 12961 MW; D633320FC7E3F3E6 CRC64;

Query Match 17.6%; Score 140; DB 5; Length 118;  
 Best Local Similarity 28.9%; Pred. No. 1.5e-05;  
 Matches 43; Conservative 25; Mismatches 33; Indels 48; Gaps 8;  
 OY 3 LASGVSIADECTAFNDRMSGNKANKT-KFLIFKADNKKKEVIDEVSQEDYEVRSL 61

DB 1 MASGCVDENCVARNNEL-----KIRKTYKWIIVFKIENTK--IIVE----- 39  
 OY 62 LEATDSDGN-----PAP--RYAVDVEYDLGGEGKRSKIYFISWVSDPTLTSM 111  
 DB 40 ----RDGKNADDFRGALPANDCFRAVINC-----GNKIOFVLMCPDNAPVRRPM 85  
 OY 112 IYASTRENLNALNITHTSI--HADDKDI 138  
 DB 86 TYASSKDALKKLDGATAVALEAHEMGDL 114

Search completed: January 29, 2002, 18:46:18  
 Job time: 1771 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 29, 2002, 18:18:07 ; Search time 186.23 Seconds  
(without alignments)  
30.319 Million cell updates/sec

Title: US-09-722-838-2  
Sequence: 1 MALASGVSTADICTAFNDF.....KGDIEKTYLAEASGSKACK 154

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues  
Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	286	35.9	143	1	COF1_YEAST
2	246	30.9	137	1	COF1_SCHPO
3	201.5	25.3	137	1	ACTP_ACACA
4	190.5	23.9	166	1	COF1_CHICK
5	189.5	23.8	166	1	COF1_MOUSE
6	188.5	23.7	166	1	COF1_HUMAN
7	188.5	23.7	166	1	COF1_RAT
8	188.5	23.7	166	1	COF2_HUMAN
9	188.5	23.7	166	1	COF2_MOUSE
10	185.5	23.3	166	1	COF1_PIG
11	168	21.1	139	1	ADP_LILLO
12	163.5	20.5	168	1	COF2_XENLA
13	160.5	20.2	168	1	COF1_XENLA
14	158	19.8	139	1	ADP_MAIZE
15	154.5	19.4	137	1	COF1_DICDI
16	152.5	19.2	152	1	ADP2_CAEEL
17	149	18.7	165	1	DEST_CHICK
18	144	18.1	165	1	CADF_DROME
19	140	17.6	165	1	DEST_HUMAN
20	136.5	17.1	126	1	ADP_BRANA
21	128	16.1	165	1	ADP1_CAEEL
22	100	12.6	146	1	P17_DICDI
23	83	10.4	141	1	GLMB_HUMAN
24	83	10.4	141	1	GLMB_RAT
25	82	10.3	158	1	HSB3_DROME
26	79.5	10.0	499	1	HSB2_TOBAC
27	77.5	9.7	332	1	TWRI_YEAST
28	77.5	9.7	731	1	HS9A_HUMAN
29	76	9.5	1059	1	NKRA_TRYBB
30	75	9.4	1906	1	SPS_VICFA
31	74	9.3	281	1	KMLS_CHICK
32	73.5	9.2	637	1	YTXC_BACSU
33	73.5	9.2	637	1	MUTA_PROPR

34	73.5	9.2	835	1	VP3_ROT51	P15736 stam1n 11 x
35	73.5	9.2	1142	1	PAK1_YEAST	P38990 saccharomyc
36	73	9.2	329	1	DHOA_EMENI	P25415 emericella
37	73	9.2	719	1	TOPI_MYCA	Q9165 mycoplasma
38	73	9.2	726	1	HS9A_BRARE	Q00474 brachydanio
39	72.5	9.1	413	1	YTHS_ECOLI	P32140 escherichia
40	72.5	9.1	533	1	SWAL_SCHPO	P32834 schizosacch
41	72	9.0	621	1	SRPR_YEAST	P22916 saccharomyc
42	72	9.0	632	1	PAKE_HAETN	P43703 haemophilus
43	72	9.0	699	1	HSB2_ORYSA	P33126 oryza sativ
44	72	9.0	1772	1	MSPI_PLAYO	P13828 plasmodium
45	71.5	9.0	442	1	TAGC_BACSU	P27622 bacillus su

## ALIGNMENTS

RESULT	ID	COF1_YEAST	STANDARD	PRT	143 AA
AC	Q03048				
DT	01-JUL-1993	(Rel. 26, Created)			
DT	01-JUL-1993	(Rel. 26, Last sequence update)			
DT	20-AUG-2001	(Rel. 40, Last annotation update)			
DE	COFILIN				
GN	COF1 OR YIL050C				
OS	Saccharomyces cerevisiae (Baker's yeast).				
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;				
OX	Saccharomycetales; Saccharomycetaceae; Saccharomycetes.				
NCBI_TaxID=4932;					
[1]					
SEQUENCE FROM N.A., AND SEQUENCE OF 43-56; 83-98 AND 106-141.					
MEMLINE=93132073; PubMed=8421056;					
Moon A.L., Janney P.A., Louie K.A., Drubin D.G.;					
"Cofilin is an essential component of the yeast cortical					
cytoskeleton.";					
J. Cell Biol. 120:421-435(1993).					
[2]					
SEQUENCE FROM N.A.					
MEMLINE=93178959; PubMed=8440472;					
Iida K., Moriyama K., Matsumoto S., Kawasaki H., Nishida E.,					
Yahara I.;					
"Isolation of a yeast essential gene, COF1, that encodes a homologue					
of mammalian cofilin, a low-M(r) actin-binding and depolymerizing					
protein.";					
Gene 124:115-120(1993).					
[3]					
SEQUENCE FROM N.A.					
Wedler H., Medler E., Scharfe M., Wambutt R.;					
Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.					
[4]					
X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).					
MEMLINE=97290449; PubMed=9145106;					
Fedorov A.A., Lappalainen P., Fedorov E.V., Drubin D.G., Almo S.C.;					
"Structure determination of yeast cofilin.";					
Nat. Struct. Biol. 4:366-369(1997).					
-1- FUNCTION: CONTROLS REVERSIBLY ACTIN POLYMERIZATION AND					
DEPOLYMERIZATION IN A PH-SENSITIVE MANNER. IT HAS THE ABILITY TO					
BIND G- AND F-ACTIN IN A 1:1 RATIO OF COFILIN TO ACTIN. IT IS THE					
MAJOR COMPONENT OF INTRACLEAR AND CYTOPLASMIC ACTIN RODS. IN					
EFFECT, YEAST COFILIN INCREASES THE RATE OF ACTIN POLYMERIZATION					
BY MAKING NEW ENDS AVAILABLE FOR ACTIN SUBUNIT ADDITION. SUCH A					
PROTEIN COMPLEX IS IMPORTANT FOR THE POLARIZED GROWTH OF YEAST					
CELLS.					
-1- SUBCELLULAR LOCATION: THROUGHOUT THE CYTOPLASM (BUT NOT ON THE					
CYTOPLASMIC CABLES) AND MAJOR COMPONENT OF THE CORTICAL ACTIN					
CYTOSKELETON.					
-1- PTR: THE N-TERMINUS IS BLOCKED.					
-1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.					
SIMILAR TO THE N-TERMINUS OF YEAST ABPI PROTEIN.					
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RL J. Biol. Chem. 273:25106-25111(1998).
CC -1- FUNCTION: FORMS A ONE TO ONE COMPLEX WITH MONOMERIC ACTIN. CAN
CC REGULATE THE POOL AVAILABLE FOR POLYMERIZATION. SEVERAL ACTIN
CC FILAMENTS IN A DOSE-DEPENDENT MANNER.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M3361; AAA02909.1; -.
DR PDB; 1AHQ; 04-SEP-97.
DR PDB; 1CND; 01-JUN-99.
DR InterPro: IPR003264; Actin_depolymrzng.
DR InterPro: IPR002108; Cofilin_ADF.
DR Pfam; PF00241; Cofilin_ADF; 1.
DR ProDom; PD002129; Cofilin_ADF; 1.
DR SMART; SM00102; ADF; 1.
DR PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.
DR Actin-binding; 3D-structure.
KW INT_MET 0
FT MOD_RES 1 1 BLOCKED.
FT DOMAIN 86 105 ACTIN-BINDING (POTENTIAL).
SQ SEQUENCE 137 AA; 15422 MW; D16030A4EF6347B CRC64;

Query Match 25.3%; Score 201.5; DB 1; Length 137;
Best Local Similarity 31.0%; Pred. No. 2.1e-12;
Matches 45; Conservative 34; Mismatches 51; Indels 15; Gaps 6;

QY 5 SGVSIADCEITAFNDFRMSGNKANKTKFIIRKIDNKEVYIDEV-SCQEDYEVRSLRLE 63
DB 1 SGIVSDCCVCKVELKL-----GHQRIYVTRKMANSTEEVVEHVGGNATYEDFSQL- 55
QY 64 ATKSKGNAPRAYVYDYEDYDLGGGGRSKRTIVFISWPSDTPLTMSMIVASTRENLNA 123
DB 56 PERCC-----RYALFDEFPQVDGQ--RNKITFILMAPDAPIKSKMNYSTKSIKK 107
QY 124 L-NHTSIHADKGDIEKTVLAER 147
DB 108 LVGIQVEQATDAEISQDAVSERA 132

RESULT 4
COFL_CHICK STANDARD; PRT; 166 AA.
ID COFL_CHICK STANDARD; PRT; 166 AA.
AC P21566;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE COFILIN.
OS Gallus gallus (Chicken).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
CC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=91027755; PubMed=1699599;
RA Abe H., Endo T., Yamamoto K., Obinata T.;
RT "Sequence of cDNA encoding actin depolymerizing factor and cofilin
RT actin-regulatory proteins exhibit high structural homology.";
RL Biochemistry 29:7420-7425(1990).
CC -1- FUNCTION: CONTROLS REVERSIBLY ACTIN POLYMERIZATION AND
DEPOLYMERIZATION IN A PH-SENSITIVE MANNER. IT HAS THE ABILITY TO

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CC BIND G- AND F-ACTIN IN A 1:1 RATIO OF COFILIN TO ACTIN. IT IS THE
CC MAJOR COMPONENT OF INTRANUCLEAR AND CYTOPLASMIC ACTIN RODS.
CC -1- SUBCELLULAR LOCATION: INTRANUCLEAR AND CYTOPLASMIC; ALMOST
CC COMPLETELY IN NUCLEUS IN CELLS EXPOSED TO HEAT SHOCK OR 10%
CC DIMETHYL SULFOXIDE.
CC -1- TISSUE SPECIFICITY: WIDELY DISTRIBUTED IN VARIOUS TISSUES.
CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M5659; AAA62732.1; -.
DR PIR; B35703; B35703.
DR HSSP; P18282; 1AK7.
DR InterPro: IPR003264; Actin_depolymrzng.
DR InterPro: IPR002108; Cofilin_ADF.
DR Pfam; PF00241; Cofilin_ADF; 1.
DR PRINTS; PR00006; COFILIN.
DR ProDom; PD002129; Cofilin_ADF; 1.
DR SMART; SM00102; ADF; 1.
DR PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.
KW Nuclear protein; Actin-binding; Cytoskeleton; Phosphorylation.
FT DOMAIN 30 34 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 106 125 ACTIN-BINDING (POTENTIAL).
FT MOD_RES 24 24 PHOSPHORYLATION (POTENTIAL); MAY PREVENT
FT RECOGNITION OF THE NUCLEAR LOCALIZATION
SQ SEQUENCE 166 AA; 18662 MW; D007B54F6A30118 CRC64;

Query Match 23.9%; Score 190.5; DB 1; Length 166;
Best Local Similarity 29.3%; Pred. No. 3e-11;
Matches 48; Conservative 33; Mismatches 58; Indels 25; Gaps 6;

QY 3 LASGVSIADCEITAFNDFRMSGNKA-----NKTFTIIRKIDNKEVYIDEVSO----- 51
DB 1 MASGVTVNDEVYIKVNDKMRKRSSTPEIKRKRRKLCISDPRKQIIVEATRLVGD 60
QY 52 ----EEDYEVRSLRLEARKDSGNAPRAYVYDYEDYDLGGGGRSKRTIVFISWPSDPT 107
DB 61 GDYVEDPYTAF-VKLLPLNDG-----RYALDADYET--KSKKEDLVETFWAPESAPL 111
QY 108 LMSMIVASTRENLKNAI-NHTSIHADKGDIEKTVLAESGG 150
DB 112 KSKMIVASSKDAIKKKFTGIRKHEQVNGLDIDKDKSTLGEKLG 155

RESULT 5
COFL_MOUSE STANDARD; PRT; 166 AA.
ID COFL_MOUSE STANDARD; PRT; 166 AA.
AC P18780;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE COFILIN, NON-MUSCLE ISOFORM.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SWISS WEBSTER;
RX MEDLINE=90272419; PubMed=2349104;
RA Moriyama K., Matsumoto S., Mishiida E., Sakai H., Yahara I.;
RT "Nucleotide sequence of mouse cofilin cDNA.";
RL Nucleic Acids Res. 18:3053-3053(1990).
CC -1- FUNCTION: CONTROLS REVERSIBLY ACTIN POLYMERIZATION AND

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CC      DEPOLYMERIZATION IN A PH-SENSITIVE MANNER. IT HAS THE ABILITY TO
CC      BIND G- AND F-ACTIN IN A 1:1 RATIO OF COFILIN TO ACTIN. IT IS THE
CC      MAJOR COMPONENT OF INTRANUCLEAR AND CYTOPLASMIC ACTIN RODS.
CC      -1- SUBCELLULAR LOCATION: INTRANUCLEAR AND CYTOPLASMIC; ALMOST
CC      COMPLETELY IN NUCLEUS IN CELLS EXPOSED TO HEAT SHOCK OR 10%
CC      DIMETHYL SULFOXIDE.
CC      -1- TISSUE SPECIFICITY: WIDELY DISTRIBUTED IN VARIOUS TISSUES.
CC      -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
CC      -----
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CC      or send an email to license@isb-slb.ch).
CC      -----
CC      EMBL; D00472; BAA00364.1; -.
CC      DR      PIR; J00201; J00201.
CC      DR      PIR; S12582; S12584.
CC      DR      HSSP; P18282; IAK7.
CC      DR      MGD; MGI:101757; Cf11.
CC      DR      InterPro; IPR003264; Actin.depolymerng.
CC      DR      InterPro; IPR002108; Cofilin_ADF.
CC      DR      Pfam; PF00241; Cofilin_ADF.1.
CC      DR      PRINTS; PR00006; Cofilin.
CC      DR      ProDom; PD002129; Cofilin_ADF.1.
CC      DR      SMART; SM00102; ADF.1.
CC      DR      PROSITE; PS00325; ACTIN.DEPOLYMERIZING.1.
CC      KW      Nuclear protein; Actin-binding; Cytoskeleton; Phosphorylation.
CC      FT      DOMAIN 30 34 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
CC      FT      DOMAIN 106 125 ACTIN-BINDING (POTENTIAL).
CC      FT      MOD_RES 24 24 PHOSPHORYLATION (POTENTIAL); MAY PREVENT
CC      FT      RECOGNITION OF THE NUCLEAR LOCALIZATION
CC      FT      SIGNAL).
CC      SQ      SEQUENCE 166 AA; 18559 MW; 19834E8CA80747B2 CRC64;
CC
QY      Query Match 23.8%; Score 189.5; DB 1; Length 166;
QY      Best Local Similarity 30.1%; Pred. No. 3.7e-11;
QY      Matches 50; Conservative 35; Mismatches 56; Indels 25; Gaps 7;
QY      3 LASGSIADECTTANDFRMSGNKA-----NKTFLIFKIANKKKEVIDE-----V 49
QY      1 MASGVAVDGYATKYNVDKMKRKSSTPEEYKRRKKAVLPCLSDKKNIILIEGKEIIVGV 60
QY      50 SQ--EDYEVERSRRLKTRKDSKGNPAPRYAVYDVEYDGGEGSKRSKIVTISWSDPT 107
QY      61 GQTVDDPPTTFEYKML-PRKDC-----RYALDATYET--KESKEDLVFIWPAENAPL 111
QY      108 LMSMITYASTRENLKAL-NIHSHADDKGDIEMKTVTLAASGKA 152
QY      112 KSKMIYASSKDAIKKKLTGIKHEILOANCYEEVKDRCTIAEKGGSA 157
QY      |||||:::| | | | : : : : : : : : : : || | | |
QY      Db 61 GQTVDDPPTTFEYKML-PRKDC-----RYALDATYET--KESKEDLVFIWPAENAPL 111
QY      108 LMSMITYASTRENLKAL-NIHSHADDKGDIEMKTVTLAASGKA 152
QY      |||||:::| | | | : : : : : : : : : : || | | |
Db 112 KSKMIYASSKDAIKKKLTGIKHEILOANCYEEVKDRCTIAEKGGSA 157
Db |||||:::| | | | : : : : : : : : : : || | | |
RESULT 6
COFL_HUMAN
ID COFL_HUMAN STANDARD: PRT: 166 AA.
AC P23528;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE COFILIN, NON-MUSCLE ISOFORM.
GN Cofilin OR Cfl.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Placenta;
EX MEDLINE=91088330; PubMed=2263493;
XA Ogawa K., Tashima M., Yumoto Y., Okuda T., Sawada H., Okuma M.,

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RA Maruyama Y.: "Coding sequence of human placenta cofilin cDNA."
RL Nucleic Acids Res. 18:7169-7169(1990).
RN (2)
RP SEQUENCE FROM N.A.
RA der Steege G., Draaijers T.G., Grootscholten P.M., Osinga J.,
RA Anzevino R., Veldora I., Brahe C., Scheffer H., van Ommen G.J.B.,
RA Buys C.H.C.M.:
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96393663; PubMed=8800436;
RA Gillett G.T., Fox M.F., Rowe P.S.N., Casimir C.M., Povey S.:
RT "Mapping of human non-muscle type cofilin (Cpl1) to chromosome 11q13
and muscle-type cofilin (Cpl2) to chromosome 14."
RL Ann. Hum. Genet. 60:201-211(1996).
CC -!- FUNCTION: CONTROLS REVERSIBLY ACTIN POLYMERIZATION AND
CC DEPOLYMERIZATION IN A PH-SENSITIVE MANNER. IT HAS THE ABILITY TO
CC BIND G- AND F-ACTIN IN A 1:1 RATIO OF COFILIN TO ACTIN. IT IS THE
CC MAJOR COMPONENT OF INTRAPLASMIC AND CYTOSOLIC ACTIN RODS.
CC -!- SUBCELLULAR LOCATION: INTRAPLASMIC AND CYTOSOLIC. ALMOST
CC COMPLETELY IN NUCLEUS IN CELLS EXPOSED TO HEAT SHOCK OR 10%
CC DIMETHYL SULFOXIDE.
CC -!- TISSUE SPECIFICITY: WIDELY DISTRIBUTED IN VARIOUS TISSUES.
CC -!- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
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CC -----
DR EMBL; D00682; BA00589.1; -
DR EMBL; U21909; AA064501.1; -
DR EMBL; X93404; CA064685.1; -
DR PIR; S12632; S12632.
DR HSSP; P18282; 1AK7.
DR Aarhus/Ghent-2DPAGE; 4; IEF.
DR MIM; 601442; -
DR InterPro; IPR003264; Actin_depolymerizing.
DR InterPro; IPR002108; Cofilin_ADF.
DR Pfam; PF00241; Cofilin_ADF.1.
DR PRINTS; PR00006; COFILIN.
DR ProDom; PD002129; Cofilin_ADF.1.
DR SMART; SM00102; ADF.1.
DR PROSITE; PS00325; ACTIN_DEPOLYMERIZING.1.
DR Nucleic Protein; Actin-binding; Cytoskeleton; Phosphorylation.
RW DOMAIN 30 34 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 106 125 ACTIN-BINDING (POTENTIAL).
FT MOD_RES 24 24 PHOSPHORYLATION (POTENTIAL); MAY PREVENT
FT RECOGNITION OF THE NUCLEAR LOCALIZATION
FT SIGNAL).
SQ
SEQUENCE 166 AA; 18502 MW; 589EF8FC1EC13719 CRC64;

Query Match 23.7%; Score 188.5; DB 1; Length 166;
Best Local Similarity 30.1%; Pred. No. 4.6e-11;
Matches 50; Conservative 34; Mismatches 57; Indels 25; Gaps 7;

QY 3 LASGVSIADECITAFNDFRMSGNKA-----NKTKEIFIKIADNKKVEYID-----V 49
DB 1 MASGVAASVDGYIYKVPNDMKVKRKSSTPEVKKRKKAVLPCLSDDKKNIILEBEKELIVGY 60
QY 50 SQ--EEDYEVFRSRLEATKDSKGNAPRYAVYDVEYDLDGSGEGRKSKYVFIISWPSDPT 107
DB 61 GQVDDPAPATFEVKML-PDKDC-----RYALYDAYET--RESKEDLVFTFMAESAPL 111
QY 108 LMSWYASTRENINKAL-NHTSIHADDKGDIEMKTVLAASGGA 152
DB 112 KSKMYYASSKDAIKKKLTGKIHLEQANVEYECYKDCSTIAEKLGGSA 157

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RESULT 7
COF1_RAT 7
ID COF1_RAT STANDARD: PRT: 166 AA.
AC P45592;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE COFILIN, NON-MUSCLE ISOFORM.
GN CFL1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=WISTAR; TISSUE=Brain;
RA Shirasawa T., Takahashi H., Sakamoto K., Kawashima A., Akashi T.;
RL Submitted (OCT-1991) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CONTROLS REVERSIBLY ACTIN POLYMERIZATION AND
CC POLYMERIZATION IN A PH-SENSITIVE MANNER. IT HAS THE ABILITY TO
CC BIND G- AND F-ACTIN IN A 1:1 RATIO OF COFILIN TO ACTIN. IT IS THE
CC MAJOR COMPONENT OF INTRANUCLEAR AND CYTOPLASMIC ACTIN RODS
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTRANUCLEAR AND CYTOPLASMIC
CC (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: WIDELY DISTRIBUTED IN VARIOUS TISSUES
CC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
CC -----
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CC -----
DR EMBL: X62908; CAA44694.1; -.
DR HSSP: P18282; 1AK7.
DR InterPro: IPR003264; Actin_depolymrznng.
DR InterPro: IPR002108; Cofilin_ADF.
DR Pfam: PF00241; cofilin_ADF; 1.
DR PRINTS: PR00006; COFILIN.
DR ProDom: PD002129; Cofilin_ADF; 1.
DR SMART: SM00102; ADF; 1.
DR PROSITE: PS00325; ACTIN_DEPOLYMERIZING; 1.
DR Nucleic protein; Actin-binding; Cytoskeleton; Phosphorylation.
FT DOMAIN 30 34 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 106 125 ACTIN-BINDING (POTENTIAL).
FT MOD_RES 24 24 PHOSPHORYLATION (POTENTIAL). MAY PREVENT
FT RECOGNITION OF THE NUCLEAR LOCALIZATION
FT SIGNAL.
SQ SEQUENCE 166 AA; 18532 MW; 19835391A81A5AB2 CRC64;

Query Match 23.7%; Score 188.5; DB 1; Length 166;
Best Local Similarity 30.1%; Pred. No. 4.6e-11;
Matches 50; Conservative 34; Mismatches 57; Indels 25; Gaps 7;

```

```

RESULT 8
COF2_HUMAN 8
ID COF2_HUMAN STANDARD: PRT: 166 AA.
AC Q9Y281;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE COFILIN, MUSCLE ISOFORM (COFILIN 2).
GN CFL2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jin J., Li G., Hu S., Li W., Yuan J., Qiang B.;
RL "Isolation of two isoforms of human cofilin cDNA."
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Nowak K.J., Biez N., Laling N.G.;
RL "Genomic sequence of the human skeletal muscle cofilin gene, CFL2."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CONTROLS REVERSIBLY ACTIN POLYMERIZATION AND
CC DEPOLYMERIZATION IN A PH-SENSITIVE MANNER. IT HAS THE ABILITY TO
CC BIND G- AND F-ACTIN IN A 1:1 RATIO OF COFILIN TO ACTIN. IT IS THE
CC MAJOR COMPONENT OF INTRANUCLEAR AND CYTOPLASMIC ACTIN RODS (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTRANUCLEAR AND CYTOPLASMIC (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF134802; AAD31280.1; -.
DR EMBL: AF134803; AAD31281.1; -.
DR EMBL: AF283513; AAF97934.1; -.
DR MIM: 601443; -.
DR InterPro: IPR003264; Actin_depolymrznng.
DR InterPro: IPR002108; Cofilin_ADF.
DR Pfam: PF00241; cofilin_ADF; 1.
DR PRINTS: PR00006; COFILIN.
DR ProDom: PD002129; Cofilin_ADF; 1.
DR SMART: SM00102; ADF; 1.
DR PROSITE: PS00325; ACTIN_DEPOLYMERIZING; 1.
DR Nucleic protein; Actin-binding; Cytoskeleton; Phosphorylation.
FT DOMAIN 30 34 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 106 125 ACTIN-BINDING (POTENTIAL).
FT MOD_RES 24 24 PHOSPHORYLATION (POTENTIAL). MAY PREVENT
FT RECOGNITION OF THE NUCLEAR LOCALIZATION
FT SIGNAL.
SQ SEQUENCE 166 AA; 18736 MW; 48B6DCCAB9FE1CC CRC64;

Query Match 23.7%; Score 188.5; DB 1; Length 166;
Best Local Similarity 29.3%; Pred. No. 4.6e-11;
Matches 48; Conservative 32; Mismatches 59; Indels 25; Gaps 6;

```

DB 112 KSKMTYASSKDAIKKKFTGKHEMOYVNGDIDKDRSTLGEKLG 155

|||||: : : : : |||: : : : : |||

RESULT 9

COF2\_MOUSE STANDARD; PRT; 166 AA.

ID COF2\_MOUSE

AC P45591;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE COFILIN, MUSCLE ISOFORM (COFILIN 2).

GN CFI2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C3H; TISSUE=Skeletal muscle;

RX MEDLINE=94253093; PubMed=8195165;

RA Ono S., Minami N., Abe H., Ohinata T.;

RT "Characterization of a novel cofilin isoform that is predominantly expressed in mammalian skeletal muscle.";

RT J. Biol. Chem. 269:15280-15286(1994).

CC -1- FUNCTION: CONTROLS REVERSIBLY ACTIN POLYMERIZATION AND DEPOLYMERIZATION IN A PH-SENSITIVE MANNER. IT HAS THE ABILITY TO BIND G- AND F-ACTIN IN A 1:1 RATIO OF COFILIN TO ACTIN. IT IS THE MAJOR COMPONENT OF INTRANUCLEAR AND CYTOPLASMIC ACTIN RODS.

CC -1- SUBCELLULAR LOCATION: INTRANUCLEAR AND CYTOPLASMIC.

CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN SKELETAL MUSCLE.

CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.

CC -----

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CC -----

DR EMBL: L29468; AAA37433.1; -

DR HSSP: P18282; IAK7.

DR MGD: MG1:101763; CFI2.

DR InterPro: IPR003264; Actin\_depolymrznz.

DR InterPro: IPR002108; Cofilin\_ADF.

DR Pfam: PF00241; cofilin\_ADF; 1.

DR PRINTS: PR00006; COFILIN\_ADF; 1.

DR ProDom: PD002129; Cofilin\_ADF; 1.

DR SMART: SM00102; ADF; 1.

DR PROSITE: PS00325; ACTIN\_DEPOLYMERIZING; 1.

DR KMW Nucleic protein; Actin-binding; Cytoskeleton; Phosphorylation.

FT DOMAIN 30 34 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

FT DOMAIN 106 125 ACTIN-BINDING (POTENTIAL).

FT MOD\_RES 24 24 PHOSPHORYLATION (POTENTIAL; MAY PREVENT RECOGNITION OF THE NUCLEAR LOCALIZATION SIGNAL).

FT SEQUENCE 166 AA; 18709 MW; 48B6D7B5AE9FE1CC CRC64;

Query Match 23.7%; Score 188.5; DB 1; Length 166;

Best Local Similarity 29.3%; Pred. No. 4.6e-11;

Matches 48; Conservative 32; Mismatches 59; Indels 25; Gaps 6;

DB 1 MASGVVNDVETKVFMDVMKRSSTQETIKRRKAVLFCISDKROIIVEAQAQIIIVGDI 60

DB 52 ----EDVEYFNRSLRATKDSKGNPARYAVYVEYDLGGEGKRSKIYFISWPSDPT 107

DB 61 GDTVEPYTSF-VKLPLNDG-----RTALVDATYET--KSKKEDVLFITAPESAPL 111

OY 108 LMSMIYASTRENKNAI-NIHRSIHADKGDIEWKTVLAESAG 150

DB 112 KSKMTYASSKDAIKKKFTGKHEMOYVNGDIDKDRSTLGEKLG 155

|||||: : : : : |||: : : : : |||

RESULT 10

COF1\_PIG STANDARD; PRT; 166 AA.

ID COF1\_PIG

AC P10668; Q29374;

DT 01-JUL-1989 (Rel. 11, Created)

DT 01-JUL-1989 (Rel. 11, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE COFILIN, NON-MUSCLE ISOFORM.

GN CFI1.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.

OX NCBI\_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC TISSUE=Brain;

RX MEDLINE=88298817; PubMed=3403546;

RA Matsuzaki F., Matsumoto S., Yahara I., Yonezawa N., Nishida E., Sakai H.;

RT "Cloning and characterization of porcine brain cofilin cDNA. Cofilin contains the nuclear transport signal sequence.";

RT J. Biol. Chem. 269:11564-11568(1994).

CC [2]

CC SEQUENCE OF 1-104 FROM N.A.

CC TISSUE=Small intestine;

CC MEDLINE=96327607; PubMed=8672129;

CC Winteroe A.K., Fredholm M., Davies W.;

CC "Evaluation and characterization of a porcine small intestine cDNA library: analysis of 839 clones.";

CC Mamm. Genome 7:509-517(1996).

CC -1- FUNCTION: CONTROLS REVERSIBLY ACTIN POLYMERIZATION AND DEPOLYMERIZATION IN A PH-SENSITIVE MANNER. IT HAS THE ABILITY TO BIND G- AND F-ACTIN IN A 1:1 RATIO OF COFILIN TO ACTIN. IT IS THE MAJOR COMPONENT OF INTRANUCLEAR AND CYTOPLASMIC ACTIN RODS.

CC -1- SUBCELLULAR LOCATION: INTRANUCLEAR AND CYTOPLASMIC; ALMOST COMPLETELY IN NUCLEUS IN CELLS EXPOSED TO HEAT SHOCK OR 10% DIMETHYL SULFOXIDE.

CC -1- TISSUE SPECIFICITY: WIDELY DISTRIBUTED IN VARIOUS TISSUES.

CC -1- MISCELLANEOUS: A DOUBLE MUTATION OF LYS-112 AND LYS-114 TO GLN PRODUCES A MUTANT WITH NO ABILITY TO DEPOLYMERIZE OR BIND F-ACTIN.

CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.

CC -----

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CC -----

DR EMBL: M20866; AAA31020.1; -

DR EMBL: F14577; CAA23134.1; -

DR PIR: A29240; A29240.

DR HSSP: P18282; IAK7.

DR InterPro: IPR003264; Actin\_depolymrznz.

DR InterPro: IPR002108; Cofilin\_ADF.

DR Pfam: PF00241; cofilin\_ADF; 1.

DR PRINTS: PR00006; COFILIN\_ADF; 1.

DR ProDom: PD002129; Cofilin\_ADF; 1.

DR SMART: SM00102; ADF; 1.

DR PROSITE: PS00325; ACTIN\_DEPOLYMERIZING; 1.

DR KMW Nucleic protein; Actin-binding; Cytoskeleton; Phosphorylation.

FT DOMAIN 30 34 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

FT DOMAIN 106 125 ACTIN-BINDING (POTENTIAL).

FT MOD\_RES 24 24 PHOSPHORYLATION (POTENTIAL; MAY PREVENT RECOGNITION OF THE NUCLEAR LOCALIZATION SIGNAL).

FT SEQUENCE 166 AA; 18709 MW; 48B6D7B5AE9FE1CC CRC64;

Query Match 23.7%; Score 188.5; DB 1; Length 166;

Best Local Similarity 29.3%; Pred. No. 4.6e-11;

Matches 48; Conservative 32; Mismatches 59; Indels 25; Gaps 6;

DB 1 MASGVVNDVETKVFMDVMKRSSTQETIKRRKAVLFCISDKROIIVEAQAQIIIVGDI 60

DB 52 ----EDVEYFNRSLRATKDSKGNPARYAVYVEYDLGGEGKRSKIYFISWPSDPT 107

DB 61 GDTVEPYTSF-VKLPLNDG-----RTALVDATYET--KSKKEDVLFITAPESAPL 111

OY 108 LMSMIYASTRENKNAI-NIHRSIHADKGDIEWKTVLAESAG 150

FT MUTAGEN 112 112 K->Q: SLIGHT MODIFICATION OF ACTIVITY.

FT MUTAGEN 114 114 R->Q: IMPAIRS INTERACTION WITH ACTIN.

SQ SEQUENCE 166 AA; 18518 MW; 589E8EC1ED12719 CRC64;  
 Query Match 23.3%; Score 185.5; DB 1; Length 166;  
 Best Local Similarity 30.1%; Pred. No. 8.9e-11;  
 Matches 50; Conservative 34; Mismatches 57; Indels 25; Gaps 7;  
 QY 3 LASGVSIADDCITAFNDFRMSGNKA-----NKTFFIETKADNKEVYIDE-----V 49  
 DB 1 MASGVAAVSDGVIAKVFNMKVRKSTPEEVKKRKAVALFCUSEDKNITILEGKEIIVGDV 60  
 QY 50 SQ--EEDYEVFRSHLEATKDSKGNPAPRYAVYDVEYDLGGEGRSKRVFISWVPSDPT 107  
 DB 61 GGVYDDPYATFVKML-PDKOC-----RYALYDPTFE--KESKEDLVFIFMAPECAPL 111  
 QY 108 LMSKIVASTRENKKNAL-NHTSHADKGDIEKVTYLAESGKA 152  
 DB 112 KSKMIVASSKDAIKKIKLGIKHELOANCYEVRKDRCTLAERLGGSA 157  
 RESULT 11  
 ADF\_LILLO STANDARD; PRT; 139 AA.  
 ID ADF\_LILLO  
 AC P30175;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 01-OCT-1994 (Rel. 30, Last annotation update)  
 DE ACTIN DEPOLYMERIZING FACTOR (ADF).  
 OS Liliium longiflorum (Trumpet Lily).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae;  
 OC Liliium.  
 NCBI\_TaxID=4690;  
 RN NCBI  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV, NELLIE WHITE; TISSUE=Pollen;  
 RX MEDLINE=93144690; PubMed=8425049;  
 RA Kim S.-R., Kim Y., An G.;  
 RT "Molecular cloning and characterization of anther-preferential cDNA  
 encoding a putative actin-depolymerizing factor.";  
 RL Plant Mol. Biol. 21:39-45(1993).  
 CC -1- FUNCTION: ACTIN-DEPOLYMERIZING PROTEIN. SEVERAL ACTIN FILAMENTS  
 (F-ACTIN) AND BINDS TO ACTIN MONOMERS (BY SIMILARITY).  
 CC -1- TISSUE SPECIFICITY: PREFERENTIALLY IN MATURE ANTHR.  
 CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.  
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 CC EMBL: 214110; CAA78483.1; -  
 DR PIR: S25061; S25061.  
 DR PIR: S30935; S30935.  
 DR HSSP: P37167; IAHQ.  
 DR InterPro: IPR003264; Actin\_depolymzng.  
 DR InterPro: IPR002108; Cofilin\_ADF.  
 DR Pfam: PF00241; Cofilin\_ADF. 1.  
 DR ProDom: PD002129; Cofilin\_ADF. 1.  
 DR SMART: SM00102; ADF. 1.  
 DR PROSITE: PS00325; ACTIN\_DEPOLYMERIZING. 1.  
 DR Actin-binding.  
 KW DOMAIN 92 111 ACTIN-BINDING (POTENTIAL).  
 FT SEQUENCE 139 AA; 16226 MW; 0B45CC67136F1A9 CRC64;  
 Query Match 21.1%; Score 168; DB 1; Length 139;  
 Best Local Similarity 29.5%; Pred. No. 3.3e-09;  
 Matches 43; Conservative 31; Mismatches 58; Indels 14; Gaps 5;

QY 4 ASGVSIADDCITAFNDFRMSGNKA-----NKTFFIETKADNKEVYIDEVSO--EEDYEVFRSL 62  
 DB 5 SSGMAVDDCEKLFKEPMLKAKRN-----FRFIVKFEKQVATVERLGPNSYDFTRECL 60  
 QY 63 EATKDSKGNPAPRYAVYDVEYDLGGEGRSKRVFISWVPSDPTLMSIYASTRENKLN 122  
 DB 61 PPNE-----CRYAVFDFDE-VTDENCQSKIFFISNPSPTSRVSRMLYASTRDRKR 112  
 QY 123 ALN-IHTSHADKGDIEKVTYLAEA 147  
 DB 113 ELDGIVQLATDPSEMSMDITIKARA 138  
 RESULT 12  
 COF2\_XENLA STANDARD; PRT; 168 AA.  
 ID COF2\_XENLA  
 AC P45593;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE COFILIN 2.  
 GN XAC2.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Piploidea; Piploidea;  
 OC Xenopodidae; Xenopus.  
 NCBI\_TaxID=8355;  
 RN NCBI  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96180281; PubMed=8603919;  
 RA Abe H., Obinata T., Minamide L.S., Bamberg J.R.;  
 RT "Xenopus laevis actin-depolymerizing factor/cofilin: a  
 phosphorylation-regulated protein essential for development.";  
 RL J. Cell Biol. 132:871-885(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Oocyte;  
 RA Wada A., Gotch Y., Nishida E.;  
 RT Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: CONTROLS REVERSIBLE ACTIN POLYMERIZATION AND  
 DEPOLYMERIZATION IN A PH-SENSITIVE MANNER. IT HAS THE ABILITY TO  
 BIND G- AND F-ACTIN IN A 1:1 RATIO OF COFILIN TO ACTIN. IT IS THE  
 MAJOR COMPONENT OF INTRACELLULAR AND CYTOPLASMIC ACTIN RODS  
 (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: INTRACELLULAR AND CYTOPLASMIC  
 (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC EMBL: U26269; AAB00539.1; -  
 DR EMBL: D38406; BAA07461.1; -  
 DR HSSP: P18282; IAK7.  
 DR InterPro: IPR003264; Actin\_depolymzng.  
 DR InterPro: IPR002108; Cofilin\_ADF.  
 DR Pfam: PF00241; Cofilin\_ADF. 1.  
 DR PRINTS: PR00006; COFILIN.  
 DR ProDom: PD002129; Cofilin\_ADF. 1.  
 DR SMART: SM00102; ADF. 1.  
 DR PROSITE: PS00325; ACTIN\_DEPOLYMERIZING. 1.  
 DR Nuclear protein: Actin-binding; Cytoskeleton; Phosphorylation.  
 KW DOMAIN 30 34 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
 FT DOMAIN 30 34  
 FT SEQUENCE 168 AA; 19120 MW; 6DBCE7F8397EDFD1 CRC64;  
 Query Match 20.5%; Score 163.5; DB 1; Length 168;

Best Local Similarity 29.3%; Pred. No. 1,1e-08;  
Matches 48; Conservative 31; Mismatches 60; Indels 25; Gaps 7;

3 LASGVSIADECITAFNDR---MSGNKRANK-TKFIIFKIANDKKEVID---EVSQ--- 51  
1 MASGVASDVYKVFENDMKVRHQLSPEAKRRKRAVFCISDCKITILEPEKELIGDVI 60

52 ----EEDYEVRSRLKATKDSKGNAPRAYVDEYDLGGGEGRSKIVFISWPSDPT 107  
61 GCNVEDPYKTFVKMLPRND-----CRYALYDALYET--KETKEDLVFVMAPEEASL 111

108 LMSMIYASTRENK-NKALNIHTSIHADKDIEMKTVLAASAG 150  
112 KSMIYASSKDAIRKRTGTGKHQMOTINTYDDINDPCNLADKLG 155

RESULT 13  
COFL\_XENLA STANDARD; PRT: 168 AA.

AC P45695;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE COFILIN 1.  
GN XACL.

OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SOURCE FROM N.A.  
RX MEDLINE-96180281; PubMed-8603919;  
RA Abe H., Obinata T., Minamide L.S., Bamberg J.R.:  
"Xenopus laevis actin-depolymerizing factor/cofilin: a  
phosphorylation-regulated protein essential for development.";  
J. Cell Biol. 132:871-885(1996).  
RT J. Cell Biol. 132:871-885(1996).  
RL J. Cell Biol. 132:871-885(1996).

-1- FUNCTION: CONTROLS REVERSIBLY ACTIN POLYMERIZATION AND  
DEPOLYMERIZATION IN A PH-SENSITIVE MANNER. IT HAS THE ABILITY TO  
BIND G- AND F-ACTIN IN A 1:1 RATIO OF COFILIN TO ACTIN. IT IS THE  
MAJOR COMPONENT OF INTRACELLULAR AND CYTOPLASMIC ACTIN RODS  
(BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: INTRACELLULAR AND CYTOPLASMIC  
(BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.

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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; U26270; AAB0540.1; .  
DR HSSP; P18282; IAK7.  
DR InterPro: IPR003264; Actin\_depolymzng.  
DR InterPro: IPR002108; Cofilin\_ADF.  
DR Pfam: PF00241; Cofilin\_ADF; 1.  
DR PRINTS; PR00006; COFILIN.  
DR PRODOM; PD002129; Cofilin\_ADF; 1.  
DR SMART; SM00102; ADF; 1.  
DR PROSITE; PS00325; ACTIN\_DEPOLYMERIZING; 1.  
KW Nuclein protein; Actin-binding; Cytoskeleton; Phosphorylation.  
FT DOMAIN 30 34 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
FT DOMAIN 106 125 ACTIN-BINDING (POTENTIAL).  
SQ SEQUENCE 168 AA; 1906 MW; F3A4D8635A683D6 CRC64;

Query Match 20.2%; Score 160.5; DB 1; Length 168;  
Best Local Similarity 28.7%; Pred. No. 2,1e-08;  
Matches 47; Conservative 32; Mismatches 60; Indels 25; Gaps 7;

3 LASGVSIADECITAFNDR---MSGNKRANK-TKFIIFKIANDKKEVID---EVSQ--- 51  
1 MASGVASDVYKVFENDMKVRHQLSPEAKRRKRAVFCISDCKITILEPEKELIGDVI 60

52 ----EEDYEVRSRLKATKDSKGNAPRAYVDEYDLGGGEGRSKIVFISWPSDPT 107  
61 GCNVEDPYKTFVKMLPRND-----CRYALYDALYET--KETKEDLVFVMAPEEASL 111

108 LMSMIYASTRENK-NKALNIHTSIHADKDIEMKTVLAASAG 150  
112 KSMIYASSKDAIRKRTGTGKHQMOTINTYDDINDPCNLADKLG 155

RESULT 14  
ADE\_MAIZE STANDARD; PRT: 139 AA.

AC P46251;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE ACTIN DEPOLYMERIZING FACTOR (ADF).  
GN ADF1.  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;  
OC Panicoidae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN [1]  
RP SOURCE FROM N.A.  
RX STRAIN=CV. A188; TISSUE=Pollen;  
MEDLINE-95232182; PubMed-7716228;  
RA Rozycka M., Lopez I., Khan S., Greenland A.J., Hussey J.:  
"A Zea mays pollen cDNA encoding a putative actin-depolymerizing  
factor.";  
Plant Physiol. 107:1011-1012(1995).  
RT Plant Physiol. 107:1011-1012(1995).  
RL Plant Physiol. 107:1011-1012(1995).

-1- FUNCTION: ACTIN-DEPOLYMERIZING PROTEIN. SEVERS ACTIN FILAMENTS  
(F-ACTIN) AND BINDS TO ACTIN MONOMERS (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.

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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; X80820; CAA56786.1; .  
DR HSSP; 003048; ICFY.  
DR MAZEDB; 113737; .  
DR InterPro: IPR003264; Actin\_depolymzng.  
DR InterPro: IPR002108; Cofilin\_ADF.  
DR Pfam: PF00241; Cofilin\_ADF; 1.  
DR PRODOM; PD002129; Cofilin\_ADF; 1.  
DR SMART; SM00102; ADF; 1.  
DR PROSITE; PS00325; ACTIN\_DEPOLYMERIZING; 1.  
KW Actin-binding.  
FT DOMAIN 92 111 ACTIN-BINDING (POTENTIAL).  
SQ SEQUENCE 139 AA; 16168 MW; 08675E0A2C92D94D CRC64;

Query Match 19.8%; Score 158; DB 1; Length 139;  
Best Local Similarity 29.7%; Pred. No. 2,9e-08;  
Matches 41; Conservative 30; Mismatches 51; Indels 16; Gaps 6;

4 ASGVASIADECITAFNDRMSGNKRANK-TKFIIFKIANDKKEVIDEVSQ--EEDYEVFRSR 61  
5 SSGIAVNDCKVAFREL-----KSRRTFRIYPRIDTMEIKVDRIGEPNGYGGPFTS 59

62 LEATKDSKGNAPRAYVDEYDLGGGEGRSKIVFISWPSDPTLMSMIYASTRENK 121  
60 LPANE-----CRYALYDLDFTT-IENCCKSKIEFFSWSPDPTARTSRKMLYASSKORRR 111



OY 122 NALN-IHTSIHADKGD1 138  
DB 112 REDDIOCEIOATDPSEM 129

```
RESULT 15
COFL_DICDI STANDARD; PRT; 137 AA.
AC P54706;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE COFILIN.
GN (COFA OR COFL) AND (COFB OR COF2).
OS Dictyostellium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX2;
RX MEDLINE=9526267; PubMed=7738034;
RA Alzawa H., Sutch K., Tsubuki S., Kawashima S., Ishii A., Yahara I.;
RT "Identification, characterization, and intracellular distribution of
RT cofilin in Dictyostellium discoideum.";
RL J. Biol. Chem. 270:10923-10932(1995).
CC -1- FUNCTION: CONTROLS REVERSIBLY ACTIN POLYMERIZATION AND
CC DEPOLYMERIZATION IN A PH-SENSITIVE MANNER. IT HAS THE ABILITY TO
CC BIND G- AND F-ACTIN IN A 1:1 RATIO OF COFILIN TO ACTIN. IT IS THE
CC MAJOR COMPONENT OF INTRANUCLEAR AND CYTOPLASMIC ACTIN RODS
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTRANUCLEAR AND CYTOPLASMIC
CC (BY SIMILARITY).
CC -1- MISCELLANEOUS: THERE ARE TWO GENES FOR COFILIN IN D. DISCOIDEUM,
CC THE ENCODE FOR IDENTICAL PROTEINS.
CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D37980; BA07198.1; -
DR EMBL: D37981; BA07199.1; -
DR HSSP: Q03048; 1CFY.
DR SWISS-2DPAGE: P54706; DICTY.
DR Dictydb: DD01059; coFA.
DR Dictydb: DD01059; coFB.
DR InterPro: IPR003264; Actin_depolymrzn.
DR InterPro: IPR002108; Cofilin_ADF.
DR Pfam: PF00241; cofilin_ADF.1.
DR ProDom: PD002129; Cofilin_ADF.1.
DR SMART: SM00102; ADF.1.
DR PROSITE: PS00325; ACTIN_DEPOLYMERIZING.1.
KW Nuclear protein; Actin-binding; Cytoskeleton; Multigene family.
SQ SEQUENCE 137 AA; 15224 MW; 0C0B0673354F46F3 CRC64;
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Query Match 19.4%; Score 154.5; DB 1; Length 137;  
Best Local Similarity 27.6%; Pred. No. 6.1e-08; Indels 27; Gaps 6;  
Matches 40; Conservative 31; Mismatches 47;  
OY 3 LASGVSIADECITAFNDRMSGNKNKTKFIIFKIDNKKKEVIDEVSQEDYEVFSRL 62  
DB 1 MSGSIALAPNCVSTFNDLKL---GRKYGIIYRISDSSEIIVD-----STL 44  
OY 63 -----EATKDSKGNPAPRYAVYDVEYDLGGEGKRSKIVFISWPSDPTLMSMIYAS 115  
DB 45 PACGSEDFEFTKCPENEC-RYVVLDTQYKEGAQ--KSKICFVAMCPDPTANIKKKMATTS 101  
OY 116 TRENLKNA-LNHTSIHADKGDIE 139

DB 102 SKDSLKACVIGIYIGCTDASEVK 126

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RESULT 16
ADF2_CAEEL STANDARD; PRT; 152 AA.
AC Q07748;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE ACTIN DEPOLYMERIZING FACTOR 2.
GN ADF-60.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Rhabditioidea;
OC Rhabdilitida; Peioderlinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150469; PubMed=8107682;
RA McKim K.S., Matheson C., Marra M.A., Makarchuk M.F., Baillie D.L.;
RT "The Caenorhabditis elegans unc-60 gene encodes proteins homologous
RT to a family of actin-binding proteins.";
RL Mol. Gen. Genet. 242:346-357(1994).
CC -1- FUNCTION: DEPOLYMERIZE GROWING ACTIN FILAMENTS IN MUSCLE CELLS;
CC REQUIRED FOR THE ASSEMBLY OF ACTIN FILAMENTS INTO THE CONTRACTILE
CC MYOFILAMENT LATTICE OF C. ELEGANS MUSCLE. MUTATIONS IN UNC-60
CC RESULT IN PARALYSIS.
CC -1- ALTERNATIVE PRODUCTS: THE TWO ISOFORMS OF UNC-60 ARE PRODUCED BY
CC ALTERNATIVE SPLICING; HOWEVER THEY ONLY SHARE AN EXON THAT CODES
CC FOR THE INITIATOR MET.
CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
CC -----
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CC -----
DR EMBL: L18963; AAC14457.1; -
DR PIR: S41727; S41727.
DR HSSP: P37167; IAH0.
DR InterPro: IPR003264; Actin_depolymrzn.
DR InterPro: IPR002108; Cofilin_ADF.
DR Pfam: PF00241; cofilin_ADF.1.
DR ProDom: PD002129; Cofilin_ADF.1.
DR SMART: SM00102; ADF.1.
DR PROSITE: PS00325; ACTIN_DEPOLYMERIZING.1.
KW Actin-binding; Alternative splicing.
FT DOMAIN 99 118 ACTIN-BINDING (POTENTIAL).
SQ SEQUENCE 152 AA; 17046 MW; BD912E2DBEAC6DE CRC64;
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Query Match 19.2%; Score 152.5; DB 1; Length 152;  
Best Local Similarity 28.4%; Pred. No. 1.1e-07; Indels 21; Gaps 7;  
Matches 44; Conservative 36; Mismatches 54;  
OY 3 LASGVSIADECITAFNDRMSGNKNKTKFIIFKIDNKKKEVIDEVSQEDYEV 57  
DB 1 MASGVKWDPSCKNAYD---LHNK-HQHSYIIIFKIDNDAIVVEKGEKNAPYAEVEE 56  
OY 58 FRSRLKATKDSKGNPAPRYAVYDVEYDL--GGEGKR--SKIVFISWPSDPTLMSMIY 113  
DB 57 MKRLVEDGKEC-----RYAAVDETVYQROGAGCTSLNKKVIVQYCPDNAPVRRRLMY 110  
OY 114 ASTRENKLNALNHT--SIHADKGDIEKTVLAE 146  
DB 111 ASSVRLKASLGLESIFQVQASMSDIDERSVKSD 145  
RESULT 17

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DEST_CHICK
ID DEST_CHICK STANDARD: PRT: 165 AA.
AC P18359:
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE DESTIN (ACTIN DEPOLYMERIZING FACTOR) (ADF).
OS Gallus gallus (Chicken).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
CC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 101-111 AND 116-134.
RC TISSUE-Brain;
RX MEDLINE=91027754; PubMed=223773;
RA Adams M.E., Minamide L.S., Diester G., Bamberg J.R.;
RT "Nucleotide sequence and expression of a cDNA encoding chick brain
RT actin depolymerizing factor."
RL Biochemistry 29:7414-7420(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Skeletal muscle;
RX MEDLINE=91027755; PubMed=1699599;
RA Abe H., Endo T., Yamamoto K., Oinata T.;
RT "Sequence of cDNAs encoding actin depolymerizing factor and cofilin
RT of embryonic chicken skeletal muscle: two functionally distinct
RT actin-regulatory proteins exhibit high structural homology."
RL Biochemistry 29:7420-7425(1990).
-1- FUNCTION: ACTIN-DEPOLYMERIZING PROTEIN. SEVERES ACTIN FILAMENTS (F-
-1- ACTIN) AND BINDS TO ACTIN MONOMERS (G-ACTIN). ACTS IN A PH-
INDEPENDENT MANNER.
-1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
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CC
CC EMBL: J02912; AAA48575.1; -
CC EMBL: M55660; AAA48573.1; -
CC PIR: A35702; A35702.
CC PIR: A35703; A35703.
CC HSSP: P18282; IAK7.
CC InterPro: IPR003264; Actin_depolymtrng.
CC InterPro: IPR002108; Cofilin_ADF.
CC Pfam: PRO0241; Cofilin_ADF; 1.
CC PRINTS: PR00006; COFILIN.
CC PRODOM: PD002129; Cofilin_ADF; 1.
CC SMART: SM00102; ADF; 1.
CC PROSITE: PS00325; ACTIN_DEPOLYMERIZING; 1.
CC Actin-binding.
CC
CC DOMAIN 30 34 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
CC FT DOMAIN 106 125 ACTIN-BINDING (POTENTIAL).
CC SEQUENCE 165 AA: 18532 MW: 75DD20D24519B629 CRC64;

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Query Match 18.7%; Score 149; DB 1; Length 165;  
 Best Local Similarity 26.8%; Pred. No. 2,6e-07;  
 Matches 44; Conservative 32; Mismatches 62; Indels 26; Gaps 7;

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OY 3 LASGSIADICTAENDPDM-----SGNKANKTKFLIEKIANDKKEVIDE----- 48
DB 1 MASGVQVADEVICRIFYDMVKRCSTPEEVYKKRKAIVICLSPDKCIIEEGKEILVGV 60
OY 49 -VSOEDEVEFSRSLRARKDSKGNAPRAVYDVYDLGGGGRKSKIVFISWVSDFPT 107
DB 61 GTVTVDPKRFHVEML-PEKDC-----RALTDSFET--KSKKEELMFLMAEQAPL 111
OY 108 LWSMVIYASTRENLMNAL-NIHTSIHADKDGIEMTKVLAEASG 150

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DB 112 KSKMIVASSKDAIKKPKQGIKHECQANGPEDLN-RACIAERLGS 154
RESULT 18
CADE_DROME STANDARD: PRT: 148 AA.
AC P45394; Q9W1C4;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE COFILIN/ACTIN DEPOLYMERIZING FACTOR HOMOLOG (D61 PROTEIN) (TWINSTAR
DE PROTEIN).
GN TSR OR CADE OR CG4254.
OS Drosophila melanogaster (Fruit fly).
CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
CC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94240181; PubMed=8183953;
RA Edwards K.A., Montague R.A., Shepard S., Edgar B.A., Erikson R.L.,
RA Kiehart D.P.;
RT "Identification of Drosophila cytoskeletal proteins by induction of
RT abnormal cell shape in fission yeast."
RL Proc. Natl. Acad. Sci. U.S.A. 91:4589-4593(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-OREGON-R;
RX MEDLINE=96095784; PubMed=8522587;
RA Gunsalus K.C., Bonaccorsi S., Williams E., Ventr F., Gatti M.,
RA Goldberg M.L.;
RT "Mutations in twinstar, a Drosophila gene encoding a cofilin/ADF
RT homologue, result in defects in centrosome migration and
RT cytokinesis."
RL J. Cell Biol. 131:1243-1259(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Bizez R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brotlier P.,
RA Butris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Kocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Honck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibbegam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Moberly C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
RA Palazzolo W., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M.C., Skupski M.P., Smith T.,
RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svrtkas R., Tector C., Turner R., Venter E., Venter A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,

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RA Williams S.M., Moodage T., Morley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.M., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 CC Science 287:2185-2195(2000).  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).  
 CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.  
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 CC -----  
 CC EMBL: 008217; AAA19856.1; -  
 DR EMBL: U24490; AAC46962.1; -  
 DR EMBL: U24676; AAC46963.1; -  
 DR EMBL: AE003462; AAF47146.1; -  
 DR HSP: P37167; IAHQ.  
 DR Flybase: FBgn0011726; tsr.  
 DR InterPro: IPR003264; Actin.depolymzng.  
 DR InterPro: IPR002108; Cofilin.ADF.  
 DR Pfam: PF00241; cofilin.ADF.1.  
 DR ProDom: PD002129; Cofilin.ADF.1.  
 DR SMART: SM00102; ADF.1.  
 DR PROSITE: PS00325; ACTIN\_DEPOLYMERIZING.1.  
 DR Actin-binding; Cytoskeleton; Nuclear protein.  
 FT DOMAIN 19 23 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
 FT DOMAIN 96 115 ACTIN-BINDING (POTENTIAL).  
 SQ SEQUENCE 148 AA; 17153 MW; 24F7216033859620 CRC64;

Query Match 18.1%; Score 144; DB 1; Length 148;  
 Best Local Similarity 28.9%; Pred. No. 6.7e-07;  
 Matches 44; Conservative 28; Mismatches 56; Indels 24; Gaps 7;

QY 3 LASGVSIADCEITAFNDFRMSGNKAKTKETIFIKIADNKKKEVYIDEVSQEDYEVEFRSRL 62  
 DB 1 MASGVYSDVCKTTEYEIR-----KDKKRRVYIYIYIDKQIDVETAYADNAEVDQFLEDI 56  
 QY 63 EATKDSKGNPAP-RIAYVDEY---DLGGGE-GRSKYIFISVPSDTPPLMSMTIASTR 117  
 DB 57 Q-----KCGPGECRYGLFPEYWHQCGTSSSSKKOKFLFMSWCPTAKYKKMYLSSSF 111  
 QY 118 ENLKNAAL-NHTSIHADKGDIEKTVLAESAS 148  
 DB 112 DALKSLVGVOXYIQATD-----LSEAS 134

RESULT 19  
 DEST\_HUMAN 19  
 ID DEST\_HUMAN STANDARD; PRT; 165 AA.  
 AC P18282;  
 DR 01-NOV-1990 (Rel. 16, Created)  
 DR 01-NOV-1990 (Rel. 16, Last sequence update)  
 DR 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE DESKRIN (ACTIN DEPOLYMERIZING FACTOR) (ADF).  
 GN ACTDP.  
 OS Homo sapiens (Human), and Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606, 9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES-Human; TISSUE-Brain;  
 RX MEDLINE=94002009; PubMed=8399167;  
 RA Hawkins M., Pope B., Maciver S.K., Weeds A.G.;  
 RT "Human actin depolymerizing factor mediates a pH-sensitive  
 RT destruction of actin filaments.";  
 RL Biochemistry 32:9985-9993(1993).

RN [2]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 53-69 AND 96-112.  
 RC SPECIES-Pig; TISSUE-Brain;  
 RX MEDLINE=90202824; PubMed=2156828;  
 RA Moriyama K., Nishida E., Yonezawa N., Sakai H., Matsumoto S.,  
 RA Iida K., Yahara I.;  
 RT "Deskrin, a mammalian actin-depolymerizing protein, is closely  
 RT related to cofilin. Cloning and expression of porcine brain deskrin  
 RT cDNA.";  
 RL J. Biol. Chem. 265:5768-5773(1990).  
 RN [3]  
 RP STRUCTURE BY NMR.  
 RC SPECIES-Pig;  
 RX MEDLINE=96270507; PubMed=8674111;  
 RA Hatanaka H., Ogura K., Moriyama K., Ichikawa S., Yahara I.,  
 RA Inagaki F.;  
 RT "Tertiary structure of deskrin and structural similarity between two  
 RT actin-regulating protein families.";  
 RL Cell 85:1047-1055(1996).  
 CC -1- FUNCTION: ACTIN-DEPOLYMERIZING PROTEIN. SEVERS ACTIN FILAMENTS (F-  
 CC ACTIN) AND BINDS TO ACTIN MONOMERS (G-ACTIN). ACTS IN A PH-  
 CC INDEPENDENT MANNER.  
 CC -1- TISSUE SPECIFICITY: WIDELY DISTRIBUTED IN VARIOUS TISSUES.  
 CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.  
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 CC -----  
 CC EMBL: S65738; AAB28361.1; -  
 DR EMBL: D90053; BAA14105.1; -  
 DR PIR: A35179; A35179.  
 DR PIR: A54184; A54184.  
 DR PDB: 1AK6; 12-OCT-97.  
 DR PDB: 1AK7; 15-OCT-97.  
 DR InterPro: IPR003264; Actin.depolymzng.  
 DR InterPro: IPR002108; Cofilin.ADF.  
 DR Pfam: PF00241; cofilin.ADF.1.  
 DR PRINTS: PR00006; COFILIN.  
 DR ProDom: PD002129; Cofilin.ADF.1.  
 DR SMART: SM00102; ADF.1.  
 DR PROSITE: PS00325; ACTIN\_DEPOLYMERIZING.1.  
 DR Actin-binding; 3D-structure.  
 FT DOMAIN 30 34 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
 FT DOMAIN 106 125 ACTIN-BINDING (POTENTIAL).  
 SQ SEQUENCE 165 AA; 18506 MW; 8668A3167924100E CRC64;

Query Match 17.6%; Score 140; DB 1; Length 165;  
 Best Local Similarity 26.2%; Pred. No. 1.8e-06;  
 Matches 43; Conservative 33; Mismatches 62; Indels 26; Gaps 7;

QY 3 LASGVSIADCEITAFNDFRMSGNKA-----NKTIFITFKIADNKKKEVYIDE----- 48  
 DB 1 MASGVYADCEYCRIFDYMKYKCTSTPEIKRKAIVIFCLSDAKCITVEGKEIIVGDV 60  
 QY 49 -VSGEDYEYFRSLKLETKOSKGNPAPRIAYVDEYDLGGGEGGRSKYIFISVPSPTPT 107  
 DB 61 GVTITDFPKHFVGNL-DEKCC-----RYALYDSFET--KESKRELMFFLAPL 111  
 QY 108 LMSVYASTRENKNAAL-NHTSIHADKGDIEKTVLAESASG 150  
 DB 112 KSKMIVASKDAIKKKGKIGKHEQANGPEDLN-RACIAKELG 154

RESULT 20  
 ADF\_BRANA 20  
 ID ADF\_BRANA STANDARD; PRT; 126 AA.  
 AC P30174;

```

DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE ACTIN DEPOLYMERIZING FACTOR (ADF) (FRAGMENT).
OS Brassica napus (Rape).
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
CC eutrosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Anther;
RX MEDLINE=93144690; Pubmed=8425049;
RA Kim S.-R., Kim Y., An G.;
RT "Molecular cloning and characterization of anther-preferential cDNA
RT encoding a putative actin-depolymerizing factor.";
RL Plant Mol. Biol. 21:39-45(1993)
CC -1- FUNCTION: ACTIN-DEPOLYMERIZING PROTEIN. SEVERS ACTIN FILAMENTS
CC (F-ACTIN) AND BINDS TO ACTIN MONOMERS (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: PREFERENTIALLY IN MATURE ANTHER.
CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Z14109; CAA78482.1; -
DR PIR: S25059; S25059.
DR PIR: S30934; S30934.
DR HSSP: P37167; IAHQ.
DR InterPro: IPR003264; Actin_depolymrzn.
DR InterPro: IPR002108; Cofilin_ADF.
DR Pfam: PF00241; Cofilin_ADF.1.
DR ProDom: PD002129; Cofilin_ADF.
DR SMART: SM00102; ADF.1.
DR PROSITE: PS00325; ACTIN_DEPOLYMERIZING; 1.
KW Actin-binding.
KW Actin-binding.
FT DOMAIN 1 98 ACTIN-BINDING (POTENTIAL).
FT SEQUENCE 126 AA; 14798 MW; EA4B26BFE387A3 CRC64;
SQ

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Query Match 17.1%; Score 136.5; DB 1; Length 126;  
 Best Local Similarity 28.6%; Pred. No. 2.8e-06;  
 Matches 40; Conservative 32; Mismatches 49; Indels 19; Gaps 7;

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QY 11 DECITAFNDFRMSGNKANKTKFIIFKIDNKKEVVIDEV-SQEDYEYFRSRLEATKDSK 69
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 2 DCKLKFEL-----KKRIFRIFRIRI--DGOQVVEKLGNGQERYDDFTASLPDE--- 51
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 70 GNPARYAVYDEVYDLGGEG-KRSKIYFISWPSDTPLMSMTIYASTRENKALN-1H 127
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 52 ---CRYAVFD--FDFTNNENQCKSKIFFIAWSPDSRYRMKMYAVASSKDRKRLDGIQ 105
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 128 TSHADKGDIEKMTVLAEA 147
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 106 VELQATDPSEMSFDITIKSRA 125

```

RESULT 21  
 ADF1\_CAEEL STANDARD; PRT; 165 AA.  
 AC Q07750;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 01-OCT-1994 (Rel. 30, Last annotation update)  
 DE ACTIN DEPOLYMERIZING FACTOR 1.  
 GN UNC-60.  
 OS Caenorhabditis elegans.

```

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150469; Pubmed=8107682;
RA McKim K.S., Matheson C., Marra M.A., Wakarchuk M.F., Baillie D.L.;
RT "The Caenorhabditis elegans unc-60 gene encodes proteins homologous
RT to a family of actin-binding proteins.";
RL Mol. Gen. Genet. 242:346-357(1994).
CC -1- FUNCTION: DEPOLYMERIZE GROWING ACTIN FILAMENTS IN MUSCLE CELLS;
CC REQUIRED FOR THE ASSEMBLY OF ACTIN FILAMENTS INTO THE CONTRACTILE
CC MYOFILAMENT LATTICE OF C.ELEGANS MUSCLE. MUTATIONS IN UNC-60
CC RESULT IN PARALYSIS.
CC -1- ALTERNATIVE PRODUCTS: THE TWO ISOFORMS OF UNC-60 ARE PRODUCED BY
CC ALTERNATIVE SPLICING; HOWEVER THEY ONLY SHARE AN EXON THAT CODES
CC FOR THE INITIATOR MET.
CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L18963; AAC14458.1; -
DR PIR: S41728; S41728.
DR HSSP: P37167; IAHQ.
DR InterPro: IPR003264; Actin_depolymrzn.
DR InterPro: IPR002108; Cofilin_ADF.
DR Pfam: PF00241; Cofilin_ADF.1.
DR ProDom: PD002129; Cofilin_ADF.
DR SMART: SM00102; ADF.1.
DR PROSITE: PS00325; ACTIN_DEPOLYMERIZING; 1.
KW Actin-binding; Alternative splicing.
KW Actin-binding.
FT DOMAIN 111 130 ACTIN-BINDING (POTENTIAL).
FT SEQUENCE 165 AA; 18367 MW; AB4F8D983BF8508E CRC64;
SQ

```

Query Match 16.1%; Score 128; DB 1; Length 165;  
 Best Local Similarity 27.8%; Pred. No. 2.5e-05;  
 Matches 47; Conservative 32; Mismatches 66; Indels 24; Gaps 10;

```

QY 3 LASGVSIADCEITAFNDFRMSGNKANKTKFIIFKIDNKKEVVID-EVSOE-----EDY 55
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1 MSSGVMVDPDVGTSQKL-SEGRK--EYRIIFKIDENK--YIVSAAYQDGLGTGDY 55
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 56 E-----VFRSLRLEATKDSKGNAP-RYAVYDEVYD---LGGEGRSKRVFTSWPSDTP 106
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 56 DSSRAAFDPKFEVDKVSRTDNLTDRCYAVFDFKFTCSRGAAGTSKMDKIIFQICPDGAS 115
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 107 TLMSMIYASTRENKALN1H--TSHADKGDIEKMTVLAASGKGAK 153
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 116 IKKKWYVASSAAAIKTSIGTKIIFQVDSSEMSHKEILNKL-GEKYG 163
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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RESULT 22  
 P17\_DICDI STANDARD; PRT; 146 AA.  
 AC P34121;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE CYTOSKELETAL P17 PROTEIN (COACTOSIN) (CYCLIC AMP-REGULATED PROTEIN P16).  
 GN P17.  
 OS Dictyostelium discoideum (Slime mold).  
 CC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.  
 OX NCBI\_TaxID=44689;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 128-133.

```

RC STRAIN=AX2;
RX MEDLINE=94123348; PubMed=8293475;
RA De Hosios E.L., Bradtke B., Lottspeich F., Gerisch G.;
RT "Coactosin", a 17 kDa F-actin binding protein from Dictyostelium
RL Cell Motil. Cytoskeleton 26:181-191(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AX3;
RA Sastry R., Abbruzzo G., Tauber A.I.;
RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: BINDS TO F-ACTIN IN A CALCIUM INDEPENDENT MANNER. BINDS
CC TO THE FILAMENTS ALONG THEIR LENGTH.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- PTM: THE N-TERMINUS IS BLOCKED.
CC -1- SIMILARITY: SOME, TO DREBRINS, COFILINS, AND YEAST ABP1.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X6197; CAA3899.1; -
DR EMBL: M82992; AAA33174.1; -
DR PIR: S1711; S1711.
DR SWISS-2DPAGE: P34121; DICTY.
DR DictyDb: DD01050; -
DR InterPro: IPR002108; Cofilin_ADF.
DR Pfam: PF00241; cofilin_ADF; 1.
DR SMART: SM00102; ADF; 1.
DR Cytoskeleton: Actin-binding.
DR SMART: SM00102; ADF; 1.
SQ SEQUENCE 146 AA; 16004 MW; EE7AE2432D8FE1D9 CRC64;

Query Match 12.6%; Score 100; DB 1; Length 146;
Best Local Similarity 27.2%; Pred. No. 0.0099;
Matches 37; Conservative 25; Mismatches 42; Indels 32; Gaps 7;

QY 27 ANKTKEIFRIADNKEKVID-----EVSQEDYEYFRSLRLEATKDSKNPAPRYAV 78
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 20 SNTNMLCFYV-BGKNKIYVLSGKSGSFALAEIN-----QPESELVA 62
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 79 YDVEYDLGGEGEGRSKIVFISWPSDTPTV-----WSMTIYSTRENILKN-ALNHTSIHAD 133
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 63 Y-LRVVSGDESRKRFVFSWCGEEVGPLAKANVSVKASVKQVINKIGVEHYTV-AD 120
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 134 DKGDIEMKTYLAEASG 149
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 121 DLNEELMTKVRKSSG 136

RESULT 23
GLMB_HUMAN STANDARD; PRT; 141 AA.
AC P17774;
QY 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE GLIA MATURATION FACTOR BETA (GMF-BETA).
GN GMFB.
OS Homo sapiens (Human), and Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBL_TaxID=9606, 9913;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Human;
RX MEDLINE=91303115; PubMed=1712830;
RA Kaplan R., Zahner A., Jaye M., Lim R.;
RT "Molecular cloning and expression of biologically active human glia

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RT maturation factor-beta.";
RL J. Neurochem. 57:483-490(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=Human; TISSUE=Brain;
RA Saito T., Tanaka N., Toyomasu T.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE.
RC SPECIES=Bovine;
RX MEDLINE=90319086; PubMed=2196564;
RA Lim R., Zahner A., Lane W.S.;
RT "Complete amino acid sequence of bovine glia maturation factor beta.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:5233-5237(1990).
RN [4]
RP PHOSPHORYLATION.
RC SPECIES=Human;
RX MEDLINE=95321959; PubMed=7598724;
RA Lim R., Zahner A.;
RT "Phorbol ester stimulates rapid intracellular phosphorylation of glia
RT maturation factor.";
RL Biochem. Biophys. Res. Commun. 211:928-934(1995).
CC -1- FUNCTION: THIS PROTEIN CAUSES DIFFERENTIATION OF BRAIN CELLS,
CC STIMULATION OF NEURAL REGENERATION, AND INHIBITION OF
CC PROLIFERATION OF TUMOR CELLS.
CC -1- PHOSPHORYLATED; STIMULATED BY PHORBOL ESTER.
CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY. GMF
CC SUBFAMILY.
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CC -----
DR EMBL: M86492; AAA58614.1; -
DR EMBL: AB001106; BAB19232.1; -
DR PIR: A33066; JDBOB.
DR PIR: PT0410; PT0410.
DR MIM: 601713; -
DR InterPro: IPR002108; Cofilin_ADF.
DR Pfam: PF00241; cofilin_ADF; 1.
DR SMART: SM00102; ADF; 1.
DR Growth factor; Acetylation; Phosphorylation.
FT INIT_MET 0
FT MOD_RES 1 1 ACETYLATION.
SQ SEQUENCE 141 AA; 16582 MW; EED4AF200E2F370 CRC64;

Query Match 10.4%; Score 83; DB 1; Length 141;
Best Local Similarity 24.5%; Pred. No. 0.39;
Matches 34; Conservative 20; Mismatches 63; Indels 22; Gaps 6;

QY 9 IADECTIAFNDFRMSGKAKKTKFIIFKIDNKEKYIDE-----VDSQEDYEYFRSLRLEA 64
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 9 VAEDLVKLRKFRP--RKTNNMAIIMKIDKRLVYLDLELGISDFE----- 55
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 65 TSKSGNPAPRYAVYDVEYDLGGEGEGRS-KIVFISWPSDTPTLMSMTIYSTRENILKN 123
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 56 LKDELPERGRFIVYSKYQ--HDDGRVSYPLCFIPSPVGCAPEDQMMYAGSKNNLYQR 113
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 124 LNIHTSIHADKGDIT--EW 140
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 114 AELTKVFEIRNTEDLNEEW 132

RESULT 24
GLMB_RAT STANDARD; PRT; 141 AA.
AC Q63228;
QY 01-NOV-1997 (Rel. 35, Created)

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DB 10 MSGNKKVKKQOQVLMILDSKNKIKYDVTITTEGKESSEKELMOKNKSNGCYSDPEPRH 69
QY 77 AV-----YDEVYDLGEGEGRSKI-VFISWVPSDPTPLMSIYATRENKLNALNI 126
DB 70 PLPPOLFENDEYCGDADFAMANEIDPLEYFLKLAPADT-TAVSTAQIEIKQENGDAKKE 128
QY 127 HTSIHADK-----GDIEKMTYLA 146
DB 129 EAETEAEDKKTEAGDGDVYKEBAE 154

RESULT 26
HS82_TOBAC STANDARD; PRT; 499 AA.
ID HS82_TOBAC STANDARD; PRT; 499 AA.
AC P36182;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE HEAT SHOCK PROTEIN 82 (FRAGMENT).
GN HSP82.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=CV. SAMSUN;
RA Severin K., Rottke R., Behrens H., Heller P., Schoeffl F.;
RL Submitted (NOV-1991) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: MOLECULAR CHAPERONE. HAS ATPASE ACTIVITY
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.
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CC -----
DR EMBL: X63195; CAA44877.1; -
DR PIR: S18865; S18865.
DR InterPro: IPR001404; HSP90.
DR Pfam: PF00183; HSP90; 1.
DR PROSITE: PS00298; HSP90; PARTIAL.
KW Chaperone; ATP-binding; Heat shock.
FT NON_TER 1
SQ SEQUENCE 499 AA; 58021 MW; D7F3C6BC48FEF003 CRC64;

Query Match 10.0%; Score 79.5; DB 1; Length 499;
Best Local Similarity 24.8%; Pred. No. 4.1;
Matches 33; Conservative 21; Mismatches 40; Indels 39; Gaps 5;
QY 31 KTLIFKADNKKKEVYDEVYDLGEGEGRSKIVFISWVPSDPTPLMSIYATRENKLNALNI 90
DB 1 EFISYPLWTEKTEKTEKESDDED-----EPKKEDEG-----AVEVEDKEKREK 47
QY 91 KRKSIYFISWVPSDPTPLMSI-----YASTREKLNALNIHSTI-H 131
DB 48 KKKRIEVSHE-----WQLINKORPIWLKPEEITKDEYASFYSLTNDWEHLAVKH 100
QY 132 ADDKGDIEMKTVL 144
DB 101 FSVEGQLEFKAIL 113

RESULT 27
TWFL_YEAST

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ID TWFL_YEAST STANDARD; PRT; 332 AA.
AC P53250;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE TWINFILIN A.
GN TWFL OR YGR080M.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN (1)
RP SEQUENCE FROM N.A.
RA Wedler H., Scharfe M., Wedler E., Wambutt R.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RX CHARACTERIZATION. PubMed-9700161;
RX MEDLINE=98365467;
RA Goode B.L., Drubin D.G., Lappalainen P.;
RT "Regulation of the cortical actin cytoskeleton in budding yeast by
RT twinfilin, a ubiquitous actin monomer-sequestering protein.";
RT J. Cell Biol. 142:723-733(1998).
CC -1- FUNCTION: ACTIN-MONOMER SEQUESTERING PROTEIN INVOLVED IN REGULATION
CC OF THE CORTICAL ACTIN CYTOSKELETON. PREVENTS ACTIN FILAMENT
CC ASSEMBLY BY FORMING A 1:1 COMPLEX WITH ACTIN MONOMERS. AND
CC INHIBITS THE NUCLEOTIDE EXCHANGE REACTION OF ACTIN MONOMERS.
CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
CC CC
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CC -----
DR EMBL: Z72865; CAA97082.1; -
DR SGD: S0003312; TWFL.
DR InterPro: IPR002108; Cofilin_ADF.
DR Pfam: PF00241; cofilin_ADF; 2.
DR SMART: SM00102; ADF; 2.
KW Actin-binding; Repeat.
SQ SEQUENCE 332 AA; 37071 MW; D9213BBB2D953DBD CRC64;

Query Match 9.7%; Score 77.5; DB 1; Length 332;
Best Local Similarity 22.6%; Pred. No. 3.8;
Matches 33; Conservative 23; Mismatches 65; Indels 25; Gaps 4;
QY 1 MALASGVSIADDECITAFNDFRMSGNKKRKFIFKADNKKVEYDEVSEDEYEVFRS 60
DB 1 MSTOSGIVADQALHSHSINE-----NLSADGIYITAKISPDSTSV-----HOTVARS 48
QY 61 RLEATKDSKGNPAPRAYVDEVYDLGEGEGRSKIVFISWVPSDPTPLMSIYATRENKL 120
DB 49 FEELVQLASQERRELYIFYRPE-----GLDKYFFVSFIPODSPYRSRLVASTNTL 100
QY 121 -----KNALNIHSTHADKGDIEK 141
DB 101 ARQGVSNLSLSTEQPLTYDADLDVYLK 126

RESULT 28
HS9A_HUMAN STANDARD; PRT; 731 AA.
ID HS9A_HUMAN STANDARD; PRT; 731 AA.
AC P07900;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HEAT SHOCK PROTEIN HSP 90-ALPHA (HSP 86).
GN HSPCA OR HSPC1 OR HSP90A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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GN NRKA.  
OS Trypanosoma brucei brucei.  
OC Eukaryota; Euzoenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
OX NCBI\_TaxID=5702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ETRO 164 / ISOLATE ISTARI;  
RX MEDLINE=93295429; PubMed=8515773;  
RA Gale M.J. Jr., Parsons M.;  
RT "A Trypanosoma brucei gene family encoding protein kinases with  
RT catalytic domains structurally related to Nekl and NIMA."  
RL Mol. Biochem. Parasitol. 59:111-122(1993).  
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN -> ADP + A PHOSPHOPROTEIN.  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.  
-----  
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-----  
CC EMBL: I03778; AAB59252.1; -  
DR HSSP: P24941; 1A01.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR001849; PH.  
DR InterPro: IPR002290; Ser\_thr\_kin\_actsite.  
DR Pfam: PF00169; PH; 1.  
DR Pfam: PF00069; pkinase; 1.  
DR SMART: SM00203; PH; 1.  
DR SMART: SM00220; S\_TKc; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS50003; PH\_DOMAIN; 1.  
KW Transferase; Serine/threonine-protein kinase; ATP-binding.  
FT DOMAIN 20 279 PROTEIN KINASE.  
FT NP\_BIND 331 429 PH.  
FT BINDING 26 34 ATP (BY SIMILARITY).  
FT ACT\_SITE 147 147 ATP (BY SIMILARITY).  
FT VARIANT 192 192 A -> P (IN STRAIN TREU66).  
FT VARIANT 199 199 K -> L (IN STRAIN TREU66).  
SQ SEQUENCE 431 AA; 47915 MW; 2E68B7027584224 CRC64;

Query Match 9.7%; Score 77; DB 1; Length 431;  
Best local Similarity 32.9%; Pred. No. 5.9;  
Matches 25; Conservative 10; Mismatches 13; Indels 28; Gaps 5;

QY 36 KIADNRKEVVIDEVSQ--EDYEVFRSRLEATKDSKGNPARYAVDYED-----LG 86  
DB 295 RIDSVDKEVLVTQVS-----EILSS--EVSPPD-----AHRELVSOINVDYTHRGHVNLKLG 342  
QY 87 GEGGRSKIVFISWVP 102  
DB 343 GGNGK-----SWKP 351

RESULT 30  
SPS\_VICFA  
ID SPS\_VICFA STANDARD; PRT; 1059 AA.  
AC Q43876;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, last sequence update)  
DT 20-AUG-2001 (Rel. 40, last annotation update)  
DE SUCROSE-PHOSPHATE SYNTHASE (EC 2.4.1.14) (UDP-GLUCOSE-FRUCTOSE-  
DE PHOSPHATE GLUCOSYLTRANSFERASE).  
GN SPS.  
OS Vicia faba (Broad bean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Vicia.  
OX NCBI\_TaxID=3906;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. FRIBO; TISSUE=Seed coat;  
RX MEDLINE=97080571; PubMed=8921916;  
RA Helm U., Weber H., Mobus U.;  
RT "Cloning and characterization of full-length cDNA encoding sucrose  
RT phosphate synthase from faba bean."  
RL Gene 178:201-203(1996).  
RN [2]  
RP SEQUENCE OF 198-314 FROM N.A.  
RC STRAIN=CV. FRIBO;  
RA Buchner P.;  
RT Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: INVOLVED IN THE REGULATION OF CARBON PARTITIONING IN  
CC THE LEAVES OF PLANTS. MAY REGULATE THE SYNTHESIS OF SUCROSE AND  
CC THEREFORE PLAY A MAJOR ROLE AS A LIMITING FACTOR IN THE EXPORT OF  
CC PHOTOSYNTHETIC PRODUCTS OUT OF THE LEAF.  
CC -1- CATALYTIC ACTIVITY: UDP-GLUCOSE + D-FRUCTOSE 6-PHOSPHATE -> UDP +  
CC SUCROSE 6-PHOSPHATE.  
CC -1- ENZYME REGULATION: ACTIVITY REGULATED BY PHOSPHORYLATION AND  
CC MODERATED BY CONCENTRATION OF METABOLITES AND LIGHT.  
CC -1- PATHWAY: SUCROSE SYNTHESIS PATHWAY.  
CC -1- SUBUNIT: HOMODIMER OR HOMOTETRAMER (BY SIMILARITY).  
CC -1- PTM: PHOSPHORYLATED. HOWEVER, PHOSPHORYLATION IS NOT ESSENTIAL FOR  
CC ENZYME FUNCTION (BY SIMILARITY).  
CC -1- SIMILARITY: SOME, WITH SUCROSE SYNTHASES.  
-----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
CC EMBL: Z56278; CAA91217.1; -  
DR EMBL: Z48640; CAA8587.1; -  
DR InterPro: IPR001296; Glycosyltransf\_1.  
DR Pfam: PF00534; Glycosyltransf\_1; 1.  
KW Transferase; Glycosyltransferase; Phosphorylation.  
SQ SEQUENCE 1059 AA; 118203 MW; FE3B49081A48EC99 CRC64;

Query Match 9.5%; Score 76; DB 1; Length 1059;  
Best local Similarity 26.3%; Pred. No. 23;  
Matches 36; Conservative 20; Mismatches 57; Indels 24; Gaps 6;

QY 34 IFRKADNRKEVVIDEVSQ--EDYEVFRSRLEATKDSKGNPARYAVDYED 83  
DB 81 IWNLARQKQLESFAVQVKNRRLERGRREATADSEDSSEGERDDP-----VSDVST 135  
QY 84 DLGGEGRSKIVFIS-----WVPSDPTLMSIRMYASTRENKLNKLNTSHADGK 136  
DB 136 H-GGGDSVKSRLPRISSADAMETWVNSQKGGKLYIVLIST-HGLIRENNMELGDSPTG 193  
QY 137 DIEWKTVLAASGGKAG 153  
DB 194 QVKYVELARALGSMPC 210

Search completed: January 29, 2002, 18:49:37  
Job time: 1890 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 29, 2002, 18:02:02 ; Search time 429.02 Seconds  
(without alignments)  
27.343 Million cell updates/sec

Title: US-09-722-838-2

Sequence: 1 MALASGVSIADICTAFNDF.....KGDIEKTVLAASGSKAGK 154

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%  
Listing first 45 summaries

Database : PIR 68:\*

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	286	35.9	143	1 A44397	cofilin - yeast (S
2	254.5	32.0	135	2 T49327	cofilin related pr
3	246	30.9	137	2 T43245	probable actin-dep
4	190.5	23.9	166	1 B35703	cofilin - chicken
5	189.5	23.8	166	1 S12584	cofilin - mouse
6	188.5	23.7	166	1 S12632	cofilin - human
7	188.5	23.7	166	2 S49101	cofilin - rat
8	188.5	23.7	166	2 A53812	cofilin, muscle -
9	185.5	23.3	166	1 A29240	cofilin - pig
10	183	23.0	142	2 S71361	actin-binding prote
11	173	21.4	140	2 A86149	hypothetical prote
12	170	21.4	139	2 T02914	actin-depolymeriz1
13	168	21.1	139	2 S30935	actin-depolymeriz1
14	164	20.6	139	2 T02883	actin-depolymeriz1
15	158	19.8	139	2 T02882	actin-depolymeriz1
16	152.5	19.2	152	2 S41727	unc-60 protein - C
17	152	19.1	132	2 G84717	actin depolymeriz1
18	150.5	18.9	293	2 T33952	actin depolymeriz1
19	150	18.8	130	2 T05788	actin-depolymeriz1
20	149	18.7	165	1 A35702	desitin - chicken
21	145	18.2	133	2 T01232	actin-depolymeriz1
22	145	18.2	164	2 JE0223	desitin - rat
23	144.5	18.2	133	2 T47539	actin depolymeriz1
24	144	18.1	148	2 A57569	actin depolymeriz1
25	140	17.6	132	2 B84543	twinstar protein -
26	140	17.6	165	1 A54184	actin depolymeriz1
27	140	17.6	165	1 A35179	desitin [validated
28	138	17.3	130	2 T47540	desitin - pig
29	136.5	17.1	126	2 S30934	actin depolymeriz1
					actin-depolymeriz1

30	128	16.1	165	2 S41728	actin depolymeriz1
31	123	15.5	130	2 T05767	actin-depolymeriz1
32	114	14.3	141	2 T37877	cofilin/tropomyos1
33	100	12.6	146	2 S17111	gene p17 protein -
34	100	12.6	328	2 T40910	probable tyrosine
35	95	11.9	350	2 A55922	cytosine kinase A6
36	93.5	11.7	149	2 S54047	hypothetical prote
37	83	10.4	141	1 JDB08	gla maturation fa
38	83	10.4	141	1 S22149	gla maturation fa
39	83	10.4	142	1 PT0410	gla maturation fa
40	82.5	10.4	419	2 T10652	hypothetical prote
41	79.5	10.0	499	2 S18865	heat shock protein
42	78	9.8	274	2 T36347	hypothetical prote
43	78	9.8	389	2 B81380	hypothetical prote
44	78	9.8	419	2 S76571	hypothetical prote
45	77.5	9.7	332	2 S64375	probable tyrosine

#### ALIGNMENTS

RESULT 1  
A44397  
cofilin - yeast (Saccharomyces cerevisiae)  
N:Alternate names: protein L0595; protein YL050c  
C:Species: Saccharomyces cerevisiae  
C>Date: 31-Dec-1993 #sequence-revision 27-Jun-1994 #text-change 21-Jul-2000  
C:Accession: A44397; B44397; JN0529; S64802; S50970; S31309; S36087  
R:Moore, A.L.; Janney, P.A.; Louie, K.A.; Drubin, D.G.  
J. Cell Biol. 120, 421-435, 1993  
A>Title: Cofilin is an essential component of the yeast cortical cytoskeleton.  
A:Reference number: A44397; M01D:93132073  
A:Accession: A44397  
A:Molecule type: DNA  
A:Residues: 1-143 <MOO>  
A:Cross-references: EMBL:Z14971; NID:93563; PIDN:CA478694.1; PID:93564  
A:Note: sequence extracted from NCBI backbone (NCBIN:122683, NCBI:P.122684)  
A:Accession: B44397  
A:Molecule type: Protein  
A:Residues: 43-56;83-96,'X',98;106-129,'DS',132-141 <MO2>  
A:Note: sequence extracted from NCBI backbone  
R:Iida, K.; Moriyama, K.; Matsumoto, S.; Kawasaki, H.; Nishida, E.; Yahara, I.  
Gene 124, 115-120, 1993  
A>Title: Isolation of a yeast essential gene, COF1, that encodes a homologue of mamma  
A:Reference number: JN0529; M01D:93178939  
A:Accession: JN0529  
A:Molecule type: DNA  
A:Residues: 1-143 <IID>  
A:Cross-references: GB:D13230; NID:9287599; PIDN:BAA02514.1; PID:9287600  
R:Wedler, H.; Wedler, E.; Scharfe, M.; Wambutt, R.  
Submitted to the Protein Sequence Database, May 1996  
A:Reference number: S64792  
A:Accession: S64802  
A:Molecule type: DNA  
A:Residues: 1-143 <MED>  
A:Cross-references: EMBL:Z73155; NID:91360250; PIDN:CA497502.1; PID:91360251; GSPDB:G  
A:Note: experimental\_source strain S288C  
R:Wedler, H.; Wambutt, R.  
Submitted to the EMBL Data Library, January 1995  
A:Description: Sequence of a 37 kb DNA fragment from chromosome XII of Saccharomyces  
A:Reference number: S50950  
A:Accession: S50970  
A:Molecule type: DNA  
A:Residues: MWGKKFTRSGENVFLCS',6-143 <MEN>  
A:Cross-references: EMBL:Z47973; NID:9642313; PIDN:CA48007.1; PID:9642314  
C:Comment: Cofilin reversibly regulates actin polymerization and depolymerization in  
C:Genetics:  
A:Gene: SGD:COF1; MIPS:YIL050c  
A:Cross-references: SGD:S0003973; MIPS:YIL050c  
A:Map position: 5/2  
A:Intons: 12L  
C:Superfamily: cofilin  
C:Keywords: actin binding



Db 112 KSKMIVASSKDAIKKKFTGKHEMVGNDLDDIKDRSTLGEKLG 155

RESULT 5  
S12584  
cofilin - mouse

C:Species: Mus musculus (house mouse)  
C:Date: 03-Feb-1994 #sequence\_revision 27-Jun-1994 #text\_change 16-Jun-2000  
C:Accession: S12584; J00201  
R:Moriyama, K.; Matsumoto, S.; Nishida, E.; Sakai, H.; Yahara, I.  
Nucleic Acids Res. 18, 3053, 1990  
A:Title: Nucleotide sequence of mouse cofilin cDNA.  
A:Reference number: S12584; MUID:90272419  
A:Accession: S12584  
A:Molecule type: mRNA  
A:Residues: 1-166 <MOR>  
A:Cross-references: EMBL:DO0472; NID:9220383; PIDN:BAA00364.1; PID:9220384  
C:Comment: Cofilin reversibly regulates actin polymerization and depolymerization in a  
C:Superfamily: cofilin  
C:Keywords: actin binding; phosphoprotein  
F:25-36/Region: nuclear location signal  
F:104-134/Region: actin binding #status predicted

Query Match 23.8%; Score 189.5; DB 1; Length 166;  
Best Local Similarity 30.1%; Pred. No. 9.7e-11;  
Matches 50; Conservative 35; Mismatches 56; Indels 25; Gaps 7;

QY 3 LASGVSIADDECITAFNDFRMSGNKA-----NKTFFIIFKIADNKKKEVIDE-----V 49

Db 1 MASGVAVSDGVYKVFNDMKVKRSSPPEVKKKKAVLFLCSEDKKNITILEGKEITVGDV 60

QY 50 SQ--EEDYEVRSRLKATKDSKGNPAPRYAYDYVDYDGGEGGKRSKTVFTSWPSPDPT 107

Db 61 GQYVDDPYTFVVKML-PDKDC-----RYALYDAYTER--KESKEDLVFTFWAPENAPL 111

QY 108 LMSMIVASTRENKLNAL-NHTSIHADDKGDIEMKTVLAESGKA 152

Db 112 KSKMIVASSKDAIKKKLTGINKHELDQANCYEVRKDRCTLAERLGS 157

RESULT 6  
S12632  
cofilin - human

C:Species: Homo sapiens (man)  
C:Date: 03-Feb-1994 #sequence\_revision 27-Jun-1994 #text\_change 16-Jun-2000  
C:Accession: S12632  
R:Ogawa, K.; Tashima, M.; Yumoto, Y.; Okuda, T.; Sawada, H.; Okuma, M.; Maruyama, Y.  
Nucleic Acids Res. 18, 7169, 1990  
A:Title: Coding sequence of human placenta Cofilin cDNA.  
A:Reference number: S12632; MUID:91088330  
A:Accession: S12632  
A:Molecule type: mRNA  
A:Residues: 1-166 <OGA>  
A:Cross-references: EMBL:DO0682; NID:9219544; PIDN:BAA00589.1; PID:9219545  
C:Comment: Cofilin reversibly regulates actin polymerization and depolymerization in a  
C:Genetics:  
A:Gene: GDB:CFIL1; CFL  
A:Cross-references: GDB:126798; OMIM:601442  
A:Map position: 11q13-11q13  
C:Superfamily: cofilin  
C:Keywords: actin binding; phosphoprotein  
F:25-36/Region: nuclear location signal  
F:104-134/Region: actin binding #status predicted

Query Match 23.7%; Score 188.5; DB 1; Length 166;  
Best Local Similarity 30.1%; Pred. No. 1.2e-10;  
Matches 50; Conservative 34; Mismatches 57; Indels 25; Gaps 7;

QY 3 LASGVSIADDECITAFNDFRMSGNKA-----NKTFFIIFKIADNKKKEVIDE-----V 49

Db 1 MASGVAVSDGVYKVFNDMKVKRSSPPEVKKKKAVLFLCSEDKKNITILEGKEITVGDV 60

QY 50 SQ--EEDYEVRSRLKATKDSKGNPAPRYAYDYVDYDGGEGGKRSKTVFTSWPSPDPT 107

Db 61 GQYVDDPYTFVVKML-PDKDC-----RYALYDAYTER--KESKEDLVFTFWAPENAPL 111

QY 108 LMSMIVASTRENKLNAL-NHTSIHADDKGDIEMKTVLAESGKA 152

Db 112 KSKMIVASSKDAIKKKLTGINKHELDQANCYEVRKDRCTLAERLGS 157

RESULT 7  
S49101  
cofilin - rat

C:Species: Rattus norvegicus (Norway rat)  
C:Date: 31-Jan-1995 #sequence\_revision 12-May-1995 #text\_change 13-Aug-1999  
C:Accession: S49101; A58860; JEO222  
R:Shirahawa, T.; Takahashi, H.; Sakamoto, K.; Kawashima, A.; Akashi, T.  
submitted to the EMBL Data Library, October 1991  
A:Description: Nucleotide sequence of rat cofilin cDNA.  
A:Reference number: S49101  
A:Accession: S49101  
A:Molecule type: mRNA  
A:Residues: 1-166 <SHI>  
A:Cross-references: EMBL:X62908; NID:9509200; PIDN:CAA44694.1; PID:9509201  
submitted to DDBJ, October 1991

A:Reference number: A58860

A:Accession: A58860

A:Molecule type: mRNA

A:Residues: 1-166 <SH2>

A:Cross-references: EMBL:X62908; NID:9509200; PIDN:CAA44694.1; PID:9509201

A:Experimental source: embryo brain

R:Kanemori, T.; Suzuki, M.M.; Titani, K.

submitted to JIPID, August 1998

A:Description: Complete amino acid sequences and phosphorylation sites, determined by

A:Reference number: JEO222

A:Accession: JEO222

A:Molecule type: protein

A:Residues: 2-166 <KAN>

C:Superfamily: cofilin

C:Keywords: acetylated amino end; phosphoprotein

F:2-166/Product: cofilin #status experimental

F:19-34/Region: nuclear location signal

F:104-115/Region: actin binding #status predicted

F:2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental

F:3/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 23.7%; Score 188.5; DB 2; Length 166;  
Best Local Similarity 30.1%; Pred. No. 1.2e-10;  
Matches 50; Conservative 34; Mismatches 57; Indels 25; Gaps 7;

QY 3 LASGVSIADDECITAFNDFRMSGNKA-----NKTFFIIFKIADNKKKEVIDE-----V 49

Db 1 MASGVAVSDGVYKVFNDMKVKRSSPPEVKKKKAVLFLCSEDKKNITILEGKEITVGDV 60





Db 60 LPANE-----CRAIYDIDDTT-IECQKSKIFFPMSPTATRSKMLYASSKDNFR 111  
 QY 122 NALN-IHTSIHADDKGDI 138  
 Db 112 RELDGIQCEIQATDPSEM 129

RESULT 16  
 S41727  
 unc-60 protein - Caenorhabditis elegans

C:Species: Caenorhabditis elegans  
 C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Nov-1999  
 C:Accession: S41727; T33953  
 R:McKimm, K.S.; Matheson, C.; Maier, M.A.; Wakarchuk, M.F.; Bailly, D.L.  
 M.O. Gen. Genet. 242, 346-357, 1994  
 A:Title: The Caenorhabditis elegans unc-60 gene encodes proteins homologous to a family  
 A:Reference number: S41727; MUID:94150469  
 A:Accession: S41727  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-152 <CMCK>  
 A:Cross-references: EMBL:L18963; NID:g304342; PIDN:AAC14457.1; PID:g516117  
 R:Courtnay, L.; Bauer, C.; Wohlman, P.  
 submitted to the EMBL Data Library, February 1999  
 A:Description: The sequence of C. elegans cosmid F53E2.  
 A:Reference number: Z21444  
 A:Accession: T33953  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-152 <COU>  
 A:Cross-references: EMBL:AF125953; PIDN:AD14705.1; GSPDB:GN00023  
 A:Experimental source: strain Bristol N2; clone F53E2  
 A:Genetics:  
 A:Gene: unc-60  
 A:Map position: 5  
 A:Introns: 29/3; 67/2; 96/2  
 C:Superfamily: cofilin

Query Match 19.2%; Score 152.5; DB 2; Length 152;  
 Best Local Similarity 28.4%; Pred. No. 2.7e-07;  
 Matches 44; Conservative 36; Mismatches 54; Indels 21; Gaps 7;  
 QY 3 LAGSVIADCTIAFNDFRMSGKANKTKFIIFKIDNKKEVIDEVSQ-----EDYEV 57  
 Db 1 MASGVKVDPSCKNAYD---LHAK-HQHSYIIFKIDKNDIAIVEKGEKNAPYAEVVE 56  
 QY 58 FRSRLKATKDSKGNPAPRYAVDYEDL--GGEGKR--SKIYFISWVSDPTLMSMT 113  
 Db 57 MKTLVEGKEC-----RYAAVDEYEVYVQGAEGSTLKNKVFVQYCPDNAPVRRRLTY 110  
 QY 114 ASTRENKALNLIHT--SIHADDKGDIEMKTVLA 146  
 Db 111 ASSVALKASLGLESLFOVQASEMSDLEKSVKSD 145

RESULT 17  
 G84717  
 actin depolymerizing factor 6 [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 16-Feb-2001  
 C:Accession: G84717  
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
 M.; Koo, H.; Moffatt, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
 euse, D.; Niemman, W.C.; White, O.; Etsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
 Nature 402, 761-768, 1999  
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
 A:Reference number: A84420; MUID:20083487  
 A:Accession: G84717  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-132 <STO>

A:Cross-references: GB:AE002093; NID:g4432815; PIDN:AAD20665.1; GSPDB:GN00139  
 C:Genetics:  
 A:Gene: At2g31200  
 A:Map position: 2  
 C:Superfamily: cofilin

Query Match 19.1%; Score 152; DB 2; Length 132;  
 Best Local Similarity 27.1%; Pred. No. 2.6e-07;  
 Matches 39; Conservative 38; Mismatches 53; Indels 14; Gaps 5;

QY 7 VSIADECTIAFNDFRMSGKANKTKFIIFKIDNKKEVIDEV--SQEDYEVFRSRLKAT 65  
 Db 1 MGVADESKTTFLEQ-----RKTHRYVVEKIDSKKEVVEKGTPTESYDDFLASLP-- 54  
 QY 66 KDSKGNPAPRYAVDYEDLGGEGKRSKIYFISWVSDPTLMSMTASTRENKALN 124  
 Db 55 -----DNDCRAVYDFDP-VTSENCKSKIFFPMSPTSGIRAKVLYSTKQDLSRLQ 108  
 QY 125 NHTSIHADDKGDIEMKTVLAAS 148  
 Db 109 GIHYELQATDPTEVLEVLRRAN 132

RESULT 18  
 T33952  
 actin depolymerizing factor homolog unc-60 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
 C:Accession: T33952  
 R:Courtnay, L.; Bauer, C.; Wohlman, P.  
 submitted to the EMBL Data Library, February 1999  
 A:Description: The sequence of C. elegans cosmid F53E2.  
 A:Reference number: Z21444  
 A:Accession: T33952  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-293 <COU>  
 A:Cross-references: EMBL:AF125953; PIDN:AD14704.1; GSPDB:GN00023; CESP:C38C3.5b  
 A:Experimental source: strain Bristol N2; clone F53E2  
 A:Genetics:  
 A:Gene: unc-60; CESP:C38C3.5b  
 A:Map position: 5  
 A:Introns: 1/3; 33/3; 109/2; 142/3; 171/3; 209/2; 238/2

Query Match 18.9%; Score 150.5; DB 2; Length 293;  
 Best Local Similarity 28.6%; Pred. No. 9.6e-07;  
 Matches 44; Conservative 35; Mismatches 54; Indels 21; Gaps 7;  
 QY 4 ASGVSIADCTIAFNDFRMSGKANKTKFIIFKIDNKKEVIDEVSQ-----EDYEV 58  
 Db 143 ASGVKVDPSCKNAYD---LHAK-HQHSYIIFKIDKNDIAIVEKGEKNAPYAEVVE 198  
 QY 59 FRSRLKATKDSKGNPAPRYAVDYEDL--GGEGKR--SKIYFISWVSDPTLMSMT 114  
 Db 199 KTLVEGKEC-----RYAAVDEYEVYVQGAEGSTLKNKVFVQYCPDNAPVRRRLTY 252  
 QY 115 STRENKALNLIHT--SIHADDKGDIEMKTVLA 146  
 Db 253 SSVALKASLGLESLFOVQASEMSDLEKSVKSD 286

RESULT 19  
 T05788  
 actin-depolymerizing factor W7J2.40 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 13-Aug-1999  
 C:Accession: T05788  
 R:Bevan, M.; Bagnues, M.; Perez-Perez, A.; Terol, J.; Torres, A.; Perez-Alonso, M.; H  
 submitted to the Protein Sequence Database, April 1998  
 A:Reference number: Z15452  
 A:Accession: T05788



```

A:Molecule type: DNA
A:Residues: 1-130 <BEV>
A:Cross-references: EMBL:AL022197
A:Experimental source: cultivar Columbia; BAC clone MJJ2
C:Genetics:
A:Map position: 4
A:Introns: 81/2
A:Note: M7J2.40
C:Superfamily: cofilin
C:Keywords: actin binding

Query Match          18.8%; Score 150; DB 2; Length 130;
Best Local Similarity 27.3%; Pred. No. 3.9e-07;
Matches 39; Conservative 38; Mismatches 50; Indels 16; Gaps 6;

QY 7 VSADICTAENDFRMSGNKANKTKFIIFKTIADNKEVVIDEV--SQEDYEVFRSLREAT 65
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1 MAVEDCEKLFKLELKSRRN----YRFLIFRI--DQGVYVEKLGMPDTYDFATSLPAN 54
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 66 KDSKGNPAPRAVYDYEDVLDGGEGSKSKIVFISWPSDPTLWSMIYASTRENKKNALN 125
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 55 E-----CRAVVEPDFE--ITDENCQKSKIFFIAMPSPSSVRMKMYAVASKDFRELD 106
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 126 -IHSHADKGDIEFKTVLAEA 147
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 107 GIOVELQATDPESEMSFDIIKSRA 129
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 20
A35702
N:destrin - chicken
N:Alternate names: actin-depolymerizing factor
C:Species: Gallus gallus (chicken)
C:Date: 12-Oct-1990 #sequence_revision 05-Aug-1994 #text_change 22-Jun-1999
C:Accession: A35702; A35703; A40672
R:Adams, M.E.; Minamide, L.S.; Duester, G.; Bamburg, J.R.
A:Title: Nucleotide sequence and expression of a cDNA encoding chick brain actin depolymerizing factor
A:Reference number: A35702; MUID:91027754
A:Accession: A35702
A:Molecule type: mRNA
A:Residues: 1-165 <ADA>
A:Cross-references: GB:J02912; NID:g211096; PIDN:AAA48575.1; PID:g211097
A:Experimental source: brain
A:Note: part of this sequence was confirmed by peptide sequencing
R:Abpe, H.; Endo, T.; Yamamoto, K.; Obinata, T.
A:Title: Sequence of cDNAs encoding actin depolymerizing factor and cofilin of embryonic chick
A:Reference number: A35703; MUID:91027755
A:Accession: A35703
A:Molecule type: mRNA
A:Residues: 1-165 <ABE>
A:Cross-references: GB:M55660; GB:J02915; NID:g211092; PIDN:AAA48573.1; PID:g211093
A:Experimental source: muscle
A:Note: part of this sequence was confirmed by peptide sequencing
R:Morgan, T.E.; Lockarbie, R.O.; Minamide, L.S.; Browning, M.D.; Bamburg, J.R.
A:Title: Isolation and characterization of a regulated form of actin depolymerizing factor
A:Reference number: A40672; MUID:93328764
A:Accession: A40672
A:Molecule type: protein
A:Residues: 20-30 <MOR>
R:Agnew, B.J.; Minamide, L.S.; Bamburg, J.R.
J: Biol. Chem. 270, 17582-17587, 1995
A:Title: Reactivation of phosphorylated actin depolymerizing factor and identification of phosphorylation sites
A:Reference number: A38989; MUID:95340558
A:Contents: annotation; acetylated amino end; phosphorylation site
C:Comment: Destrin is an actin-binding protein that is capable of rapidly depolymerizing actin
C:Superfamily: cofilin
C:Keywords: acetylated amino end; actin binding; phosphoprotein
J:2-165/Product: destrin #status predicted <MAT>

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[illegible]

	Query Match	17.6%;	Score 140;	DB 2;	Length 133;	
	Best Local Similarity	29.7%;	Pred. No. 3.se-06;			
	Matches	38;	Mismatches 47;	Indels 14;	Gaps 6;	
			Conservative			
OY	9 IAECEITAFENDFMMSGNKRANKTKFIETFKIADNKKEVVIDEV-SQEEDEYEFRRSLRLEATKD	67				
	:      :    :    :        :    :    :	51				
Dd	3 VTDECJTSSFMD--MKKKKHYH-RYIVFKIEEKSRRKYVDKGVGAGEST-----HDLED	51				
OY	68 SKGNAPRAYAVYDEVYDLGGGBGSKRSKIYFIWVSDPTPLTMSIMIVASTRENTKNAL-NI	126				
	:    :	110				
Dd	52 SLPVDDCGRIAYVEPDE-VTVDNCRKSKIFFIAMSPBASKIRAKILVATSKGLRVLEGII	110				
OY	127 HTSIHADH 134					
	:  :					
Dd	111 HYELOATFD 118					





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 29, 2002, 17:20:51 ; Search time 65.13 Seconds  
(without alignments)  
53.209 Million cell updates/sec

Title: US-09-722-838-2

Perfect score: 796  
Sequence: 1 MALMSGVIADECTAFENDF.....KGDIEKTVLAESGKAKK 154

Scoring table:  
BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08  
Maximum Match 100%  
Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/prodata/2/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/2/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/2/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/2/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/2/1aa/PCUTUS.COMB.pep:\*  
6: /cgn2\_6/prodata/2/1aa/backfil1a1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	95	11.9	350	2	US-09-123-851-3
2	95	11.9	350	2	US-08-728-520-3
3	89	11.2	350	1	US-08-184-252A-2
4	89	11.2	350	5	PCT-US95-00601-2
5	84	10.6	141	2	US-08-187-186A-5
6	83	10.4	141	2	US-08-442-497C-9
7	76.5	9.6	732	2	US-08-533-669A-18
8	73.5	9.2	343	2	US-09-123-851-1
9	73.5	9.2	343	2	US-08-728-520-1
10	71.5	9.0	1057	4	US-08-853-948B-2
11	71	8.9	425	4	US-08-960-780-27
12	71	8.9	425	4	US-09-073-898-27
13	70.5	8.9	396	1	US-08-471-791-13
14	70.5	8.9	396	5	PCT-US91-01746-13
15	70.5	8.9	885	1	US-08-484-105-14
16	70.5	8.9	885	1	US-08-484-106-14
17	69.5	8.7	1248	2	US-08-348-353-17
18	69.5	8.7	1248	2	US-08-465-965-17
19	69.5	8.7	1248	1	US-08-465-966-17
20	68	8.5	1770	1	US-08-445-135-2
21	68	8.5	1727	2	US-08-477-451-10
22	67	8.4	1045	2	US-08-553-436A-6
23	66.5	8.4	489	3	US-08-369-822C-27
24	66.5	8.4	489	3	US-08-582-776C-42
25	66.5	8.4	489	3	US-08-434-831B-39
26	66	8.3	899	4	US-09-413-814-5
27	65	8.2	186	5	PCT-US91-08177-15

28	65	8.2	323	2	US-08-747-788-2	Sequence 2, Appl1
29	65	8.2	699	2	US-08-694-865-16	Sequence 16, Appl1
30	65	8.2	699	3	US-09-124-491-16	Sequence 16, Appl1
31	65	8.2	750	4	US-09-185-160-14	Sequence 14, Appl1
32	64.5	8.1	1054	1	US-08-356-354-4	Sequence 4, Appl1
33	64.5	8.1	1054	2	US-08-778-656-4	Sequence 4, Appl1
34	64.5	8.1	1089	1	US-08-180-195-36	Sequence 36, Appl1
35	64.5	8.1	1089	1	US-08-168-917-4	Sequence 4, Appl1
36	64.5	8.1	1089	1	US-08-477-329-36	Sequence 36, Appl1
37	64.5	8.1	1089	2	US-08-475-458-36	Sequence 36, Appl1
38	64.5	8.1	1089	2	US-08-460-510-4	Sequence 4, Appl1
39	64.5	8.1	1089	2	US-08-460-490-4	Sequence 4, Appl1
40	64.5	8.1	1089	3	US-08-980-400-36	Sequence 36, Appl1
41	64.5	8.1	1089	3	US-08-462-728-2	Sequence 2, Appl1
42	64.5	8.1	1089	4	US-09-583-459A-36	Sequence 36, Appl1
43	64.5	8.1	1089	4	US-09-583-210-36	Sequence 36, Appl1
44	64.5	8.1	1089	4	US-09-583-449A-36	Sequence 36, Appl1
45	64.5	8.1	1089	5	PCT-US92-00730-4	Sequence 4, Appl1

#### ALIGNMENTS

RESULT 1  
US-09-123-851-3  
Sequence 3, Application US/09123851  
Patent No. 5958405  
GENERAL INFORMATION:  
APPLICANT: GOLI, Surya K.  
TITLE OF INVENTION: A NOVEL HUMAN PROTEIN TYROSINE KINASE  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/123,851  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/728,520  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0136 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 350 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 451482  
US-09-123-851-3

Query Match 11.9%; Score 95; DB 2; Length 350;  
Best Local Similarity 24.5%; Pred. No. 0.0023;  
Matches 36; Conservative 28; Mismatches 61; Indels 22; Gaps 5;

[illegible]

TITLE OF INVENTION: PROTEIN TYROSINE KINASE A6  
 NUMBER OF SEQUENCES: 8  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Knobbe, Martens Olson & Bear  
 STREET: 620 Newport Center Drive, Sixteenth Floor



Page 4



```

RESULT      9
US-08-728-520-1
; Sequence 1, Application US/08728520
; Patent No. 5994112
; GENERAL INFORMATION:
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: A NOVEL HUMAN PROTEIN TYROSINE KINASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTED Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/728.520
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0136 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4156
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 343 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus
;
US-08-728-520-1

Query Match          9.2%; Score 73.5; DB 2; Length 343;
Best Local Similarity 22.0%; Pred. No. 1;
Matches 33; Conservative 28; Mismatches 60; Indels 29; Gaps 7;

QY      1 MALSGVSIADCEITAFNDFPMKSGKAKKTFIIFKIDKNKKEYVIDESQE-----ED 54
      1 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      1 MAHQGHGATELEEF-----AKARAGSVRLIKVIEDXQLVLG-ASDEPPGRWD 52
      1 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY      55 YE-VFRSLERETKDSKGNPAPRYAVYDEVLDGEGGRSKIVFISVPSPTPLMSMY 113
      1 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      53 YDRAVLPFLDNO-----PCYLILRLDSQNAQ-----FEMFLFMSPDMSPVRLKMLY 101
      1 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY      114 ASTRENKNAI---NHTSHADKGDIEW 140
      1 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      102 AATRAIVKKEFGGHIKDELFGTVKVDLSF 131
      1 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

RESULT      10
US-08-853-948B-2
; Sequence 2, Application US/08853948B
; Patent No. 6210943
; GENERAL INFORMATION:
; APPLICANT: AKIHAMA, Toyota
; TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE FROM CITRUS AND DNA ENCODING
; FILE REFERENCE: 0049-0235-0

```

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      : CURRENT APPLICATION NUMBER: US/08/853,948B
      : CURRENT FILING DATE: 1997-05-09
      : NUMBER OF SEQ ID NOS: 10
      : SOFTWARE: Patentin Ver. 2.1
      : SEQ ID NO 2
      : LENGTH: 1057
      : TYPE: PRt
      : ORGANISM: Citrus unshiu
      : US-08-853-948B-2

Query Match          9.0%; Score 71.5; DB 4; Length 1057;
Best local similarity 25.0%, Pred. No. 10;
Matches 45; Conservative 24; Mismatches 60; Indels 51; Gaps 10;

QY       11 DECITAFFN-DFRMSGANKRKY-----FTIFRIADNKKEVIDESQ---E 52
        :| |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: |
Db 44     EVITGFEETDLHRSWVAQAATRSQEHNTRLENNCWIRMLNARQKQL-GEAAGRAAK 102
QY       53 EDYEVRFRRLERATKD----SKGNAPRYAYIDVYDLCG-GEGKRSLIVFSWPSOTP 106
        :| |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: |
Db 103    RLREERRRRRRTADMSEDLSGEERG-----DIVDSVAHSDSTRSRIPRISVV--DA 154
QY       107 TLMSTAVSTRENTKNALNIHTSIH-----ADDKGDTEMTKTALAEASGRAG 153
Db 155    ETW-----TSQGKKKLVIYLISHGLRGNMELGRDSPDTGGGVYVELRALDGSPG 209

RESULT 11
Sequence 27, Application US/08960780
Patent No. 620435
GENERAL INFORMATION:
APPLICANT: Feltelson, Jerald S.
APPLICANT: Schneckf, H. Ernest
APPLICANT: Narva, Kenneth E.
APPLICANT: Stockhoff, Brian A.
APPLICANT: Schmeltz, James
APPLICANT: Loewer, David
APPLICANT: Dullum, Charles Joseph
APPLICANT: Muller-Cohn, Judy
APPLICANT: Stamp, Lisa
TITLE OF INVENTION: No. 6204435el Pesticidal Toxins and Nucleotide
TITLE OF INVENTION: Sequences Which Encode These Toxins
NUMBER OF SEQUENCES: 134
CORRESPONDENCE ADDRESS:
ADDRESSEE: Salivanchik, Lloyd & Salivanchik
STREET: 2421 N.W. 41st Street, suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/M$-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,780
FILING DATE: 30-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Salivanchik, David R
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA-708
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:

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Wed Jan 30 11:57:31 2002

us-09-722-838-2.ra1

Page 6

LENGTH: 425 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: 68F  
US-08-960-780-27

Query Match 8.9%; Score 71; DB 4; Length 425;  
Best Local Similarity 24.4%; Pred. No. 2.8;  
Matches 38; Conservative 23; Mismatches 57; Indels 38; Gaps 9;

26 KANKTFIIRKIDNKEVY-----IDVSGEDYEVFRSLRATKD---SKG-----70  
155 KATKTNLITQKVKSTRDEDTDGDSDIPDIWENGCTI-QNKIAYKWDSDLSKGYTKFV 213  
71 -NPAPRAYVD--VEY-----DLGGEGKRSKIVFISWPSDPTPLMSIYASTRENILKN 122  
214 SNPLDHTVGDPTDYEKARDLDSNAKETFNPLVAAPSVNVSMEKYI-LSPDENLSN 272  
123 ALNHTSIHADKRGDIW-----KTVLAASGKAG 153  
273 SIESHSTN-----WSYNTGASIEAGGALG 300

RESULT 12

US-09-073-898-27  
Sequence 27, Application US/09073898

Patent No. 6242669  
GENERAL INFORMATION:

APPLICANT: Feltelson, Jerald S.  
APPLICANT: Schepf, H. Ernest  
APPLICANT: Narva, Kenneth E.  
APPLICANT: Stockhoff, Brian A.  
APPLICANT: Schmeits, James  
APPLICANT: Loewer, David  
APPLICANT: Dullum, Charles Joseph  
APPLICANT: Muller-Cohn, Judy  
APPLICANT: Stamp, Lisa  
APPLICANT: Morrill, George  
APPLICANT: Finstad-Lee, Stacey  
TITLE OF INVENTION: No. 6242669e1 pesticidal toxins and Nucleotide  
TITLE OF INVENTION: Sequences which Encode These Toxins  
NUMBER OF SEQUENCES: 144  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: US  
ZIP: 32606-6669

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/073,898

FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/029,848  
FILING DATE: 30-OCT-1996

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/960,780  
FILING DATE: 30-OCT-1997

ATTORNEY/AGENT INFORMATION:  
NAME: Sanders, Jay M.  
REGISTRATION NUMBER: 39,355  
REFERENCE/DOCKET NUMBER: MA-70801

TELECOMMUNICATION INFORMATION:

TELEPHONE: 352-375-8100  
TELEFAX: 352-372-5800  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 425 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: 68F  
US-09-073-898-27

Query Match 8.9%; Score 71; DB 4; Length 425;  
Best Local Similarity 24.4%; Pred. No. 2.8;  
Matches 38; Conservative 23; Mismatches 57; Indels 38; Gaps 9;

26 KANKTFIIRKIDNKEVY-----IDVSGEDYEVFRSLRATKD---SKG-----70  
155 KATKTNLITQKVKSTRDEDTDGDSDIPDIWENGCTI-QNKIAYKWDSDLSKGYTKFV 213  
71 -NPAPRAYVD--VEY-----DLGGEGKRSKIVFISWPSDPTPLMSIYASTRENILKN 122  
214 SNPLDHTVGDPTDYEKARDLDSNAKETFNPLVAAPSVNVSMEKYI-LSPDENLSN 272  
123 ALNHTSIHADKRGDIW-----KTVLAASGKAG 153  
273 SIESHSTN-----WSYNTGASIEAGGALG 300

RESULT 13

US-08-471-791-13  
Sequence 13, Application US/08471791

Patent No. 5723595  
GENERAL INFORMATION:

APPLICANT: Thompson, Gregory A  
APPLICANT: Knaut, Vic C  
TITLE OF INVENTION: Plant Desaturases-Compositions  
TITLE OF INVENTION: and Uses  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Calgene, Inc.  
STREET: 1920 Fifth Street  
CITY: Davis  
STATE: California  
COUNTRY: USA  
ZIP: 95616

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage

COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 7.1  
SOFTWARE: Microsoft Word 5.1 (a)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,791

FILING DATE: 6-JUNE-95  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/762,762  
FILING DATE: 16-SEPT-1991

CLASSIFICATION: 435  
APPLICATION NUMBER: PCT/US91/01746  
FILING DATE: 14-MAR-1991

CLASSIFICATION: 435  
APPLICATION NUMBER: 07/615,784  
FILING DATE: 14-NOV-1990

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/567,373  
FILING DATE: 13-AUG-1990

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/494,106

FILING DATE: 16-MAR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Lassen, Elizabeth  
REGISTRATION NUMBER: 31,845  
NAME: Donna E. Scherer  
REGISTRATION NUMBER: 34,719  
NAME: Carl J. Schwedler  
REGISTRATION NUMBER: 36,924  
REFERENCE/DOCKET NUMBER: CGNE 69-5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (916) 753-6313  
TELEFAX: (916) 753-1510  
TELEX: 350370 CGNE  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 396 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-471-791-13

Query Match 8.9%; Score 70.5; DB 1; Length 396;  
Best Local Similarity 20.1%; Pred. No. 2.9;  
Matches 30; Conservative 26; Mismatches 44; Indels 49; Gaps 5;

OY 36 KIADNKEVYIDVSOEE--DVEYFRSLRLEATKDSKGNPAPRAVY-----79  
DB 122 EIPDDYFVLVGDMTTEALPTVQTMNTLDGVRDETGASLTPMAVTRAWTAENRRGD 181  
OY 80 -----DVEYDGGGEGKRSKIVFISWVSDPTLMSMYASTRENL 120  
DB 182 LIHTYLVISGRVDMRQIOKTIOTYILGSGMDPRTE-----NSPYL-GFIYTSFOERA 231

OY 121 KNALNHTSIHADKGDIEKTVLAASG 149  
DB 232 TVSHGNTARHAKHDGVK----LAQICG 256

RESULT 14  
PCT-US91-01746-13  
Sequence 13, Application PC/TUS9101746  
GENERAL INFORMATION:  
APPLICANT: Thompson, Gregory A  
APPLICANT: Knaut, Vic C  
TITLE OF INVENTION: Plant Desaturases-Compositions and Uses  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Calgene, Inc.  
STREET: 1920 Fifth Street  
CITY: Davis  
STATE: California  
COUNTRY: USA  
ZIP: 95616  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB storage  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 6.0.7  
SOFTWARE: Microsoft Word 4.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/01746  
FILING DATE: 19910314  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/615,784  
FILING DATE: 14-NOV-1990  
APPLICATION NUMBER: 07/567,373  
FILING DATE: 13-AUG-1990  
APPLICATION NUMBER: 07/494,106  
FILING DATE: 16-MAR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Lassen, Elizabeth  
REGISTRATION NUMBER: 31,845

NAME: Donna E. Scherer  
REGISTRATION NUMBER: 34,719  
REFERENCE/DOCKET NUMBER: CGNE 69-3 WO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (916) 753-6313  
TELEFAX: (916) 753-1510  
TELEX: 350370 CGNE  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 396 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US91-01746-13

Query Match 8.9%; Score 70.5; DB 5; Length 396;  
Best Local Similarity 20.1%; Pred. No. 2.9;  
Matches 30; Conservative 26; Mismatches 44; Indels 49; Gaps 5;

OY 36 KIADNKEVYIDVSOEE--DVEYFRSLRLEATKDSKGNPAPRAVY-----79  
DB 122 EIPDDYFVLVGDMTTEALPTVQTMNTLDGVRDETGASLTPMAVTRAWTAENRRGD 181  
OY 80 -----DVEYDGGGEGKRSKIVFISWVSDPTLMSMYASTRENL 120  
DB 182 LIHTYLVISGRVDMRQIOKTIOTYILGSGMDPRTE-----NSPYL-GFIYTSFOERA 231

OY 121 KNALNHTSIHADKGDIEKTVLAASG 149  
DB 232 TVSHGNTARHAKHDGVK----LAQICG 256

RESULT 15  
US-08-484-105-14  
Sequence 14, Application US/08484105  
Patent No. 5589341  
GENERAL INFORMATION:  
APPLICANT: STILLMAN, Bruce  
APPLICANT: BELL, Stephen P  
APPLICANT: KOBAYASHI, Ryuji  
APPLICANT: RINE, Jasper  
APPLICANT: FOSS, Margit  
APPLICANT: McNALLY, Francis J  
APPLICANT: LAURENSEN, Patricia  
APPLICANT: HERSKOWITZ, Ira  
APPLICANT: LI, Joachim J  
APPLICANT: GAVIN, Kimberly  
TITLE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOENBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,105  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Osman Ph.D., Richard Aron  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: A-59032/DJB/BAO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 494-8700  
TELEFAX: (415) 494-8771



OY 136 GDIEKTVLAES 148  
Db 1038 GDVDRSVTRVS 1050

RESULT 18  
US-08-465-965-17  
; Sequence 17, Application US/08465965  
; Patent No. 5968512  
; GENERAL INFORMATION:  
; APPLICANT: Tuomanen, Elaine  
; APPLICANT: Masure, Robert  
; TITLE OF INVENTION: Antibody Recognizing Endothelial Cell  
; TITLE OF INVENTION: Ligand for Leukocyte CR3  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: U.S.A.  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/465,965  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/348,353  
; FILING DATE: 30-NOV-1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/247,572  
; FILING DATE: 23-MAY-1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/03725  
; FILING DATE: 04-MAY-1992  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/695,613  
; FILING DATE: 03-MAY-1991  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson, David  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 600-1-097CIPIDIV2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-487-5800  
; TELEFAX: 201-343-1684  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1248 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-465-965-17

Query Match 8.7%; Score 69.5; DB 2; Length 1248;  
Best Local Similarity 19.2%; Pred. No. 23;  
Matches 37; Conservative 27; Mismatches 72; Indels 57; Gaps 7;

OY 12 ECTAFNDFRMS---GNKAKTKTITIKIAD-----NKKEVID-----47  
Db 859 QAIIVGKDLTSLASHAGVNAEAMALMAAGELTVKAOITNKRAALIEAGGNARLTAAVA 918  
OY 48 -----EVSQEDDEVEFRSRLEATKDSKGNPAPRYAYD-----VEYDGG 87

Db 919 LNKLRIRAGEDMHLDAPIRENTAKLGE-VQRKGVQDVGSGEGRSGIGYNYMLRA 977  
OY 88 GEGRSKRVIFISWVPSDPTPTLMSI-----YASTRENKNAALN---IHTSIHADK 135  
Db 978 GNGKRKAGTIAAPWYGGDLTAESLIEVGKDLYLNAGAKDEHRLHLENGVYQAGCHGIG 1037  
OY 136 GDIEKTVLAES 148  
Db 1038 GDVDRSVTRVS 1050

RESULT 19  
US-08-465-966-17  
; Sequence 17, Application US/08465966  
; Patent No. 6013560  
; GENERAL INFORMATION:  
; APPLICANT: Tuomanen, Elaine  
; APPLICANT: Masure, Robert  
; TITLE OF INVENTION: Antibody Recognizing Endothelial Cell  
; TITLE OF INVENTION: Ligand for Leukocyte CR3  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: U.S.A.  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/465,966  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/348,353  
; FILING DATE: 30-NOV-1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/247,572  
; FILING DATE: 23-MAY-1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/03725  
; FILING DATE: 04-MAY-1992  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/695,613  
; FILING DATE: 03-MAY-1991  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson, David  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 600-1-097CIPIDIV2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-487-5800  
; TELEFAX: 201-343-1684  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1248 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-465-966-17

Query Match 8.7%; Score 69.5; DB 3; Length 1248;  
Best Local Similarity 19.2%; Pred. No. 23;  
Matches 37; Conservative 27; Mismatches 72; Indels 57; Gaps 7;



;; TITLE OF INVENTION: DNA SEQUENCES AND PLASMIDS FOR THE  
;; TITLE OF INVENTION: PREPARATION OF SUGAR BEET WITH CHANGED SUCROSE  
;; TITLE OF INVENTION: CONCENTRATION  
;; NUMBER OF SEQUENCES: 8  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Ostroienk, Faber, Gerb & Soffen  
;; STREET: 1180 Avenue of the Americas  
;; CITY: New York  
;; STATE: NY  
;; COUNTRY: US  
;; ZIP: 10036-8403  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/553,436A  
;; FILING DATE: 17-NOV-1995  
;; CLASSIFICATION: 800  
;; PRIORITY APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/EP94/01671  
;; FILING DATE: 20-MAY-1994  
;; PRIORITY APPLICATION DATA:  
;; APPLICATION NUMBER: DE P 4317596.1  
;; FILING DATE: 24-MAY-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Weillman, Edward  
;; REGISTRATION NUMBER: 24,735  
;; REFERENCE/DOCKET NUMBER: P/951-117  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 382-0700  
;; TELEFAX: (212) 382-0888  
;; TELEX: 236925  
;; INFORMATION FOR SEQ ID NO: 6:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 1045 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-553-436A-6

Query Match 8.4%; Score 67; DB 2; Length 1045;  
Best Local Similarity 21.4%; Pred. No. 35;  
Matches 36; Conservative 29; Mismatches 71; Indels 32; Gaps 7;

QY 11 DECITAFN--DFRMSGKANKTK-----FIIFKIDNKKVVIDEVSQ--EE 53  
DB 44 EEVITGEDTDLRHSVRAQATRSPOERNRLEMMCRINNLAROKOLENEEAQRTKR 103  
QY 54 DYEVSRLRLEATKDSKGNPARYAVYDVEYDLGG-GEGRSKIVFI-----SWPSDT 105  
DB 104 RMELRGREARATDMSD-----LSEGEDISAHGSDTRPLRPRISLDMETWISQOK 157  
QY 106 PTMSMIVASTRENKALNITHTSHADKGDLEWKTIVLAEASGKRG 153  
DB 158 EKRLIVLISL-HGLIRGENMELGRSDTGQYKVVVELARALGSMG 204

RESULT 23  
US-08-369-822C-27  
; Sequence 27, Application US/08369822C  
; GENERAL INFORMATION:  
; APPLICANT: Lipkin, W. I.  
; APPLICANT: Briese, Thomas  
; APPLICANT: Kliche, Stefanie  
; APPLICANT: Schneider, Patrick A.  
; APPLICANT: Stiltz, Lothar  
; APPLICANT: Schneemann, Anette  
; TITLE OF INVENTION: Borna Disease Viral Sequences,  
; TITLE OF INVENTION: Diagnostics and Therapeutics for Central Nervous

;; TITLE OF INVENTION: System Diseases  
;; NUMBER OF SEQUENCES: 46  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Fulbright & Jaworski, L.L.P.  
;; STREET: 865 South Figueroa Street, 29th floor  
;; CITY: Los Angeles  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 90017-2571  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: WINDOWS NT-WORDPERFECT 8.0  
;; SOFTWARE: ASCII (DOS) TEXT  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/369,822C  
;; FILING DATE: 06-JAN-1995  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Churchill, Margaret A. (Ph.D.)  
;; REGISTRATION NUMBER: 39,944  
;; REFERENCE/DOCKET NUMBER: 1279-194XX  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 213/680-9200  
;; TELEFAX: 213/680-4518  
;; INFORMATION FOR SEQ ID NO: 27:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 489 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; HYPOTHEICAL: NO  
;; ANTI-SENSE: NO  
;; US-08-369-822C-27

Query Match 8.4%; Score 66.5; DB 3; Length 489;  
Best Local Similarity 28.8%; Pred. No. 13;  
Matches 21; Conservative 11; Mismatches 24; Indels 17; Gaps 3;

QY 65 TKDSKGNPARYAVYDVEYDLGGEGGRSKIVFISWPSDPTPLMSMIVAS--TRENKLN 122  
DB 241 TEDRNPNPPCANAY--HYHGGIEGLQOK-----LWTCISCAQITLVLELKT 285  
QY 123 ALNHTSHADDK 135  
DB 286 KKLKSSVMGDNQ 298

RESULT 24  
US-08-582-776C-42  
; Sequence 42, Application US/08582776C  
; Patent No. 6077510  
; GENERAL INFORMATION:  
; APPLICANT: Lipkin, W. I.  
; APPLICANT: Briese, Thomas  
; APPLICANT: Kliche, Stefanie  
; APPLICANT: Schneider, Patrick A.  
; APPLICANT: Stiltz, Lothar  
; APPLICANT: Schneemann, Anette  
; TITLE OF INVENTION: Borna Disease Viral Sequences,  
; TITLE OF INVENTION: Diagnostics and Therapeutics for Central Nervous  
; TITLE OF INVENTION: System Diseases  
; NUMBER OF SEQUENCES: 61  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fulbright & Jaworski, L.L.P.  
; STREET: 865 South Figueroa Street, 29th floor  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017-2576  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: WINDOWS NT  
SOFTWARE: ASCII DOS TEXT  
CURRENT APPLICATION DATA: US/08/582,776C  
APPLICATION NUMBER: US/08-1996  
FILING DATE: 04-JAN-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: US 08/369,822  
APPLICATION NUMBER: 06-JAN-1995  
FILING DATE: 06-JAN-1995  
PRIOR APPLICATION DATA: US 08/434,831  
APPLICATION NUMBER: 04-MAY-1995  
FILING DATE: 04-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Churchill, Margaret A.  
REGISTRATION NUMBER: 39,944  
REFERENCE/DOCKET INFORMATION:  
TELEPHONE: 213/680-4518  
TELEFAX: 213/680-4518  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 489 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-582-776C-42

Query Match 8.4%; Score 66.5; DB 3; Length 489; 3;  
Best Local Similarity 28.8%; Pred. No. 13; Indels 17; Gaps 3;  
Matches 21; Conservative 11; Mismatches 24; Indels 17; Gaps 3;  
OY 65 TKDSGNPAPRYAVDYEDIGGEGKRSKIVISWPSDPTLMSIYAS--TREMLKN 122  
Db 241 TEDNRNPPDCANAY--HYHGGIEGLQK-----LWTCISCAQITLVELKT 285  
OY 123 ALNHTSIHADK 135  
Db 286 KIKKSSVWGDNQ 298

RESULT 25  
US-08-434-831B-39  
Sequence 39, Application US/08434831B  
Patent No. 611905  
GENERAL INFORMATION:  
APPLICANT: Lipkin, W. I.  
APPLICANT: Bliese, Thomas  
APPLICANT: Kliche, Stefanie  
APPLICANT: Schneider, Patrick A.  
APPLICANT: Stitz, Lothar  
APPLICANT: Schneemann, Anette  
APPLICANT: Borna Disease Viral Sequences,  
TITLE OF INVENTION: Diagnostics and Therapeutics for Central Nervous  
TITLE OF INVENTION: System Diseases  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fulbright & Jaworski, L.L.P.  
STREET: 865 South Figueroa Street, 29th Floor  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017-2571  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: WINDOWS NT--WORDPERFECT 8.0  
SOFTWARE: ASCII (DOS) TEXT  
CURRENT APPLICATION DATA: US/08/434,831B  
APPLICATION NUMBER: US/08/434,831B

FILING DATE: 04-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: US 08/369,822  
APPLICATION NUMBER: 06-JAN-1995  
FILING DATE: 06-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Churchill, Margaret A. (Ph.D.)  
REGISTRATION NUMBER: 39,944  
REFERENCE/DOCKET INFORMATION:  
TELEPHONE: 213/680-4518  
TELEFAX: 213/680-4518  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 489 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-434-831B-39

Query Match 8.4%; Score 66.5; DB 3; Length 489; 3;  
Best Local Similarity 28.8%; Pred. No. 13; Indels 17; Gaps 3;  
Matches 21; Conservative 11; Mismatches 24; Indels 17; Gaps 3;  
OY 65 TKDSGNPAPRYAVDYEDIGGEGKRSKIVISWPSDPTLMSIYAS--TREMLKN 122  
Db 241 TEDNRNPPDCANAY--HYHGGIEGLQK-----LWTCISCAQITLVELKT 285  
OY 123 ALNHTSIHADK 135  
Db 286 KIKKSSVWGDNQ 298

RESULT 26  
US-09-413-814-5  
Sequence 5, Application US/09413814  
Patent No. 6225064  
GENERAL INFORMATION:  
APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH  
APPLICANT: Bristol-Myers Squibb, Co.  
APPLICANT: Beyer, Stefan  
APPLICANT: Bloeker, Helmut  
APPLICANT: Brandt, Petra  
APPLICANT: Cino, Paul M  
APPLICANT: Dougherty, Brian A  
APPLICANT: Goldberg, Steven L  
APPLICANT: Hoffe, Gerhard  
APPLICANT: Mueller, Joachim  
APPLICANT: Reichenbach, Hans  
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polypeptide or  
TITLE OF INVENTION: heteropolypeptide compounds  
FILE REFERENCE: PCT/US 99/23535  
CURRENT APPLICATION NUMBER: US/09/413,814  
PRIOR APPLICATION DATA: 1999-10-07  
CURRENT FILING DATE: 1998-10-09  
EARLIER FILING DATE: 1998-10-09  
NUMBER OF SEQ ID NOS: 107  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 5  
LENGTH: 899  
TYPE: PRT  
ORGANISM: Sorangium cellulosum  
US-09-413-814-5

Query Match 8.3%; Score 66; DB 4; Length 899; 6;  
Best Local Similarity 19.3%; Pred. No. 37; Indels 41; Gaps 70; Gaps 6;  
Matches 32; Conservative 23; Mismatches 41; Indels 70; Gaps 6;  
OY 15 TAFNDFRMSGKNA-----NKTFIIFKTIAD-----NKREYVIDVSGEEDY 55



Db 640 TARDEKVLKIGKRLVTKIMWASKYVLSQSAEVIHISELDRALLHKLSAVYDQATRSFDE 699  
QY 56 EVFRSRLEAKRD-----SKGNAPRYAYDYDEYDGGEGGRSKYV-- 96  
Db 700 HERAAALERTEDFEWMTDAYELANARAG-----EGGAEEAANGSAVA 746  
QY 97 -----FISWPSDPTPLMSMIVASTRENKALNINHTSIH 131  
Db 747 LRLGLSVLLRFLAPVLPYITDEWWRWVYAETGD-----TSH 784

RESULT 27  
PCT-US91-08177-15  
Sequence 15, Application PC/TUS9108177  
GENERAL INFORMATION:  
APPLICANT: Samal, Silba K  
TITLE OF INVENTION: Bovine Respiratory Syncytial Virus Genes  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
STREET: 1201 New York Avenue N.W., suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/08177  
FILING DATE: 19911104  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/608,937  
FILING DATE: 05-NOV-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Highet, David W  
REGISTRATION NUMBER: 30,265  
REFERENCE/DOCKET NUMBER: 20509-96711  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4854  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 186 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US91-08177-15

Query Match 8.2%; Score 65; DB 5; Length 186;  
Best Local Similarity 17.6%; Pred. No. 4.3;  
Matches 15; Conservative 24; Mismatches 34; Indels 12; Gaps 2;  
QY 56 EVFRSRLEATKDSKGNAPRYAYVD--VEYDLGGEGGRSKYVIFISWPSDPTPLMSMIV 113  
Db 105 EINNDIKRLRNKEVPSKIRIYNTYISYDSNKRNTKQTIHLKRLPADV----- 156  
QY 114 ASTRENKALNINHTSIHADKDI 138  
Db 157 --LKTIKNTIDHNETNGNGDI 179

RESULT 28  
US-08-747-788-2  
Sequence 2, Application US/08747788  
GENERAL INFORMATION:  
APPLICANT: Ko, Kenton

APPLICANT: Pang, Peng  
TITLE OF INVENTION: ENHANCED TRANSPORT WITH A PLASTID  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.,  
STREET: Two Millitia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173-4799  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/747,788  
FILING DATE: 14-NOV-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Pearlmuter, Nina L.  
REGISTRATION NUMBER: 35,639  
REFERENCE/DOCKET NUMBER: PPL96-01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 323 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "amino acid"  
US-08-747-788-2

Query Match 8.2%; Score 65; DB 2; Length 323;  
Best Local Similarity 25.2%; Pred. No. 10;  
Matches 29; Conservative 13; Mismatches 45; Indels 28; Gaps 4;  
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Db 100 NKAMK-----EKRYAFEDVSPETTKESPFSYEEV-SETSAKRTRLFEDVLO 148  
QY 70 --GNPAPRYAYDYDEYDGGEGGRSKYVIFISWPSDPTPLMSMIVASTRENKLN 122  
Db 149 NGAPANGATASDVFOSLGAGKGMAGGSVEVLEKMIETPTQKMLYPHLPEMHN 203

RESULT 29  
US-08-694-865-16  
Sequence 16, Application US/08694865  
Patent No. 5837268  
GENERAL INFORMATION:  
APPLICANT: POTTER, ANDREW A.  
TITLE OF INVENTION: GHRH-LEUKOTOXIN CHIMERAS  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: REED & ROBINS LLP  
STREET: 285 HAMILTON AVENUE, SUITE 200  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

Wed Jan 30 11:57:31 2002

us-09-722-838-2.ra1

Page 14

APPLICATION NUMBER: US/08/694,865  
FILING DATE: 09-AUG-1996  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: MCCracken, THOMAS P.  
REGISTRATION NUMBER: 38,548  
REFERENCE/DOCKET NUMBER: 9001-0016.22  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)327-3231  
TELEFAX: (415)327-3400  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 699 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-694-865-16

Query Match 8.2%; Score 65; DB 2; Length 699;  
Best Local Similarity 24.6%; Pred. No. 33;  
Matches 43; Conservative 17; Mismatches 79; Indels 36; Gaps 6;

QY 2 ALASGVSIADECITAFNDRMSGKANKTKFIIFKIDNKEVYIDEVSOEDYEYFRSR 61  
DB 444 AIAAGVSAADLT-----FEKVKHNLVITNSKKEKVTIONMFRADFAKEVFN 492  
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DB 493 YKATKDEKIEIIGONGERITSKQVDDLAKNGKITODELSKYVDNYELLKHSKNVTNS 552  
QY 105 TPTLMSIYASTREN-LKNALNHTSIHAD-----KGDIEKTYLAASGK 151  
DB 553 LDKLISSVSAFTSSNDSRNVLVAPTSMDQSLSLQFARGSQHWSYGLRPGSGSQ 607

RESULT 30  
US-09-124-491-16  
Sequence 16, Application US/09124491  
Patent No. 6022960

GENERAL INFORMATION:  
APPLICANT: POTTER, ANDREW A.  
APPLICANT: MANN, JOHN G.  
TITLE OF INVENTION: GNRH-LEUKOTOXIN CHIMERAS  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESS: REED & ROBINS LLP  
STREET: 285 HAMILTON AVENUE, SUITE 200  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94301

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/09/124,491  
APPLICATION NUMBER: US/09/124,491

FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/694,865  
FILING DATE: 09-AUG-1996  
APPLICATION NUMBER: US 08/387,156  
FILING DATE: 10-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/960,932  
FILING DATE: 14-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/779,171  
FILING DATE: 16-OCT-1991  
ATTORNEY/AGENT INFORMATION:

NAME: MCCracken, THOMAS P.  
REGISTRATION NUMBER: 38,548  
REFERENCE/DOCKET NUMBER: 9001-0016.22  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)327-3231  
TELEFAX: (415)327-3400  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 699 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-124-491-16

Query Match 8.2%; Score 65; DB 3; Length 699;  
Best Local Similarity 24.6%; Pred. No. 33;  
Matches 43; Conservative 17; Mismatches 79; Indels 36; Gaps 6;

QY 2 ALASGVSIADECITAFNDRMSGKANKTKFIIFKIDNKEVYIDEVSOEDYEYFRSR 61  
DB 444 AIAAGVSAADLT-----FEKVKHNLVITNSKKEKVTIONMFRADFAKEVFN 492  
QY 62 LEATKDSK-----GNPAPRYAVYDYEDLGGEGR-----RSKIV-----FISWVPSD 104  
DB 493 YKATKDEKIEIIGONGERITSKQVDDLAKNGKITODELSKYVDNYELLKHSKNVTNS 552  
QY 105 TPTLMSIYASTREN-LKNALNHTSIHAD-----KGDIEKTYLAASGK 151  
DB 553 LDKLISSVSAFTSSNDSRNVLVAPTSMDQSLSLQFARGSQHWSYGLRPGSGSQ 607

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Job time: 3432 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 29, 2002, 17:17:51 ; Search time 578.26 Seconds  
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19.727 Million cell updates/sec

Title: US-09-722-838-2

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	183	23.0	139	21	AAAG35931
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3	177	22.2	139	21	AAAG05740
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5	177	22.2	150	21	AAAG04372
6	175	22.0	146	21	AAAG24917
7	175	22.0	146	21	AAAG24916
8	173	21.7	140	21	AAAG05222
9	172	21.6	150	21	AAAG22715
10	171	21.5	121	21	AAAG22716
11	169	21.2	132	21	AAAG35932

12	169	21.2	139	21	AAAG11684	Arabidopsis thalia
13	169	21.2	178	21	AAAG7844	Arabidopsis thalia
14	165	20.7	132	21	AAAG24918	Arabidopsis thalia
15	165	20.7	137	21	AAAG49077	Arabidopsis thalia
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17	163	20.5	132	21	AAAG04373	Arabidopsis thalia
18	163	20.5	132	21	AAAG05741	Arabidopsis thalia
19	163	20.5	132	21	AAAG10071	Arabidopsis thalia
20	163	20.5	137	21	AAAG3642	Arabidopsis thalia
21	163	20.5	146	21	AAAG3641	Arabidopsis thalia
22	162	20.4	146	21	AAAG29384	Arabidopsis thalia
23	159	20.0	127	21	AAAG03978	Human secreted pro
24	159	20.0	133	21	AAAG05223	Arabidopsis thalia
25	159	20.0	133	21	AAAG7448	Arabidopsis thalia
26	159	20.0	140	21	AAAG1968	Arabidopsis thalia
27	159	20.0	170	21	AAAG1987	Arabidopsis thalia
28	158	19.8	139	21	AAAG15709	Arabidopsis thalia
29	158	19.8	139	21	AAAG7862	Arabidopsis thalia
30	158	19.8	176	21	AAAG5708	Arabidopsis thalia
31	158	19.8	176	21	AAAG7861	Arabidopsis thalia
32	155	19.5	132	21	AAAG11685	Arabidopsis thalia
33	155	19.5	132	21	AAAG7845	Arabidopsis thalia
34	152	19.1	132	21	AAAG29385	Arabidopsis thalia
35	151.5	19.0	112	21	AAAG54417	Zea mays protein f
36	151.5	19.0	161	21	AAAG54415	Zea mays protein f
37	151	19.0	130	21	AAAG49078	Arabidopsis thalia
38	150	18.8	130	21	AAAG30740	Arabidopsis thalia
39	149.5	18.8	143	21	AAAG19800	Arabidopsis thalia
40	149.5	18.8	143	21	AAAG3203	Arabidopsis thalia
41	149	18.7	130	21	AAAG3643	Arabidopsis thalia
42	148.5	18.7	123	21	AAAG4938	Zea mays protein f
43	148.5	18.7	125	21	AAAG4937	Zea mays protein f
44	147.5	18.5	95	21	AAAG4939	Zea mays protein f
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# ALIGNMENTS

RESULT 1	AAAG35931 standard; Protein: 139 AA.
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AC	18-OCT-2000 (first entry)
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XX	Zea mays protein fragment SEQ ID NO: 43962.
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XX	
KW	Protein identification: signal transduction pathway; metabolic pathway;
KW	hybridisation assay; genetic mapping; gene expression control; promoter;
KW	terminalisation sequence; corn.
XX	
OS	Zea mays subsp. mays.
XX	
PN	EP1033405-A2.
XX	
PD	06-SEP-2000.
XX	
PF	25-FEB-2000; 2000EP-0301439.
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PR	05-MAR-1999; 99US-0123180.
PR	09-MAR-1999; 99US-0123548.
PR	23-MAR-1999; 99US-0125788.
PR	25-MAR-1999; 99US-0126264.
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PR	06-APR-1999; 99US-0128234.
PR	08-APR-1999; 99US-0128714.
PR	16-APR-1999; 99US-0129845.
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XX 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 28773.

KW Protein identification; signal transduction pathway; metabolic pathway;  
hybridisation assay; genetic mapping; gene expression control; promoter;  
termination sequence.

XX Arabidopsis thaliana.

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XX Protein identification; signal transduction pathway; metabolic pathway;  
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XX Zea mays subsp. mays.

XX EP1033405-A2.

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QY 90 GKRSKIVFISWPSDPPTMSMITYASTRENKLNALN-IHTSHADKDDIMKTVLAEAS 148
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XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence; corn.
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OS Zea mays subsp. mays.
XX
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## RESULT 14

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AC AAG24918;

DT 17-OCT-2000 (first entry)

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KW Protein identification; signal transduction pathway; metabolic pathway;  
hybridisation assay; genetic mapping; gene expression control; promoter;  
termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

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Query Match 20.5%; Score 163; DB 21; Length 132;  
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Matches 42; Conservative 33; Mismatches 45; Indels 16; Gaps 6;

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Db 108 dqlqvelqatdptemd 123

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AC 17-OCT-2000 (first entry)  
DT 17-OCT-2000 (first entry)  
XX Arabidopsis thaliana protein fragment SEQ ID NO: 8247.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 8247.  
XX Protein identification: signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX Arabidopsis thaliana.  
OS Arabidopsis thaliana.  
XX EP1033405-A2.  
XX PN  
XX 06-SEP-2000.  
XX PD  
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PF 25-FEB-2000; 2000EP-0301439.  
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Query Match 20.5%; Score 163; DB 21; Length 132;

Best Local Similarity 30.9%; Pred. No. 9e-11; Mismatches 45; Indels 16; Gaps 6;

Matches 42; Conservative 33; Mismatches 45; Indels 16; Gaps 6;

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RESULT 20

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AAG23642;

17-OCT-2000 (first entry)

Arabidopsis thaliana protein fragment SEQ ID NO: 27026.

XX protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.

XX Arabidopsis thaliana.

OS EPI033405-A2.

PN 06-SEP-2000.

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XX 05-MAR-1999; 99US-0123180.  
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Query Match 20.5%; Score 163; DB 21; Length 137;  
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QY 63 EATRDSKGNPAPRYAVYDVEYDLGGEG-KRSKIVFISWPSDPTLMSIYASTRENLIK 121  
DB 59 ppe-----cryayvd--fdfttaenlkskflflawspdsrvmkmvyasskdrfk 109  
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RESULT 21  
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DT 17-OCT-2000 (first entry)  
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DE  
KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
OS Arabidopsis thaliana.  
XX  
PN EPI033405-A2.  
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us-09-722-838-2.rag

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Query Match 20.5%; Score 163; DB 21; Length 174;  
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DB 96 ppee-----cryayvd--fdfttaenlqsklflawspdsstvmkmnyasskdrfk 146  
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DB 147 reldgigvelqatdpsen 164

RESULT 22  
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XX AAG29384;

XX 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 34954.

KW Protein identification: signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
XX termination sequence.

XX Arabidopsis thaliana.

XX EPI033405-A2.

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PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0159293.  
PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159295.  
PR 14-OCT-1999; 99US-0159329.  
PR 14-OCT-1999; 99US-0159330.  
PR 14-OCT-1999; 99US-0159331.  
PR 14-OCT-1999; 99US-0159337.  
PR 14-OCT-1999; 99US-0159637.  
PR 18-OCT-1999; 99US-0159584.  
PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160767.  
PR 21-OCT-1999; 99US-0160768.  
PR 21-OCT-1999; 99US-0160770.  
PR 21-OCT-1999; 99US-0160814.  
PR 21-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.  
PR 25-OCT-1999; 99US-0161404.  
PR 25-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 26-OCT-1999; 99US-0161350.  
PR 26-OCT-1999; 99US-0161361.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 20.4%; Score 162; DB 21; Length 146;  
Best Local Similarity 28.1%; Pred. No. 1,4e-10;  
Matches 41; Conservative 38; Mismatches 53; Indels 14; Gaps 5;

OY 5 SGVSIDECITAFNDFRMSGNANKRKTFLIEKIDNKKVYIDDEV-SGEEDYEVFRARLE 63  
DB 13 sgmgvadeskfttleq---rkklhyvfkideskvevkeugntesyddflasp 68  
OY 64 ATKDSGNPAPRAVYDVEYDGGGGRSKITVFTSWVPSDPTLMSMIVASTRENTKNA 123  
DB 69 -----dndcryayvdfdt-vtsencqskliffawpsstgtrakvlystskdqistre 120  
OY 124 L-NIHSTSHADDKGDIEMKTVLAEAS 148  
DB 121 lqghlyelgatdplevlelvleran 146

RESULT 23  
AAG03978  
ID AAG03978 standard; Protein: 127 AA.  
XX AAG03978;  
AC  
XX  
XX 06-OCT-2000 (first entry)  
DE  
XX Human secreted protein, SEQ ID NO: 8059.  
XX  
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
KW gene therapy; chromosome mapping.  
XX  
OS Homo sapiens.  
XX  
PN EP1033401-A2.

XX 06-SEP-2000.  
PD 21-FEB-2000; 2000EP-0200610.  
XX 26-FEB-1999; 99US-0122487.  
XX (GEST ) GENSET.  
PI Dumas Milne Edwards J, Duclert A, Giordano J;  
XX WPI: 2000-500381/45.  
DR N-PSDB: AAC03984.  
XX  
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for  
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -  
PS Claim 13; SEQ ID 8059; 71pp + CD-ROM; English.  
XX  
CC The present sequence is a polypeptide encoded by one of a large number  
CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs  
CC were prepared from total human RNAs or polyA+ RNAs derived from 30  
CC different tissues. EST sequences usually correspond mainly to the 3'  
CC untranslated region (UTR) of the mRNA because they are often obtained  
CC from oligo-dT primed cDNA libraries. Such ESTs are not well suited for  
CC isolating cDNA sequences derived from the 5' ends of mRNAs and even in  
CC those cases where longer cDNA sequences have been obtained, the full 5'  
CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'  
CC ends and can therefore be used to obtain full length cDNAs and genomic  
CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and  
CC chromosome mapping procedures. They are used to obtain upstream  
CC regulatory sequences and to design expression and secretion vectors.  
SQ Sequence 127 AA;  
  
Query Match 20.08; Score 159; DB 21; Length 127;  
Best Local Similarity 30.88; Pred. No. 2.4e-10;  
Matches 40; Conservative 26; Mismatches 40; Indels 24; Gaps 6;  
  
QY 3 LASGSIADCEITAFNDRMSGNKA-----NKTFFIIFIKADNKEVYIDE-----V 49  
Db 1 masgyavsdgyikvfndmkvkxstpeevkkrkavilfcisedkknilleegkeilvgdv 60  
QY 50 SQ--EEDYEVFRSRLEATKDSKGNPAPRYAVYDVEYDLGGEGRKSKIVFISWVPSDPT 107  
Db 61 gtvddpyatvtvkmk-pdkdc-----tyalydatyet--keskkedvlfvfwapesapl 111  
QY 108 LMSMIYASTR 117  
Db 112 kskmlyassk 121  
  
RESULT 24  
ID AAG05223 standard; Protein: 133 AA.  
AC AAG05223;  
XX  
DE 17-OCR-2000 (first entry)  
XX  
XX Arabidopsis thaliana protein fragment SEQ ID NO: 1548.  
XX  
KM Protein identification; signal transduction pathway; metabolic pathway;  
KM hybridisation assay; genetic mapping; gene expression control; promoter;  
KM termination sequence.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EP1033405-A2.  
XX  
PD 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.  
XX 25-FEB-1999; 99US-0121825.  
XX 05-MAR-1999; 99US-0123180.  
XX 09-MAR-1999; 99US-0123548.  
XX 23-MAR-1999; 99US-0125788.  
XX 25-MAR-1999; 99US-0126264.  
XX 29-MAR-1999; 99US-0126785.  
XX 01-APR-1999; 99US-0127462.  
XX 06-APR-1999; 99US-0128234.  
XX 08-APR-1999; 99US-0128714.  
XX 16-APR-1999; 99US-0129845.  
XX 19-APR-1999; 99US-0130077.  
XX 21-APR-1999; 99US-0130449.  
XX 23-APR-1999; 99US-0130510.  
XX 23-APR-1999; 99US-0130891.  
XX 28-APR-1999; 99US-0131449.  
XX 30-APR-1999; 99US-0132048.  
XX 30-APR-1999; 99US-0132407.  
XX 04-MAY-1999; 99US-0132484.  
XX 05-MAY-1999; 99US-0132485.  
XX 06-MAY-1999; 99US-0132486.  
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XX 11-MAY-1999; 99US-0132863.  
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XX 14-MAY-1999; 99US-0134219.  
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XX 14-MAY-1999; 99US-0134370.  
XX 18-MAY-1999; 99US-0134768.  
XX 19-MAY-1999; 99US-0134941.  
XX 20-MAY-1999; 99US-0135124.  
XX 21-MAY-1999; 99US-0135353.  
XX 24-MAY-1999; 99US-0135629.  
XX 25-MAY-1999; 99US-0136021.  
XX 27-MAY-1999; 99US-0136399.  
XX 28-MAY-1999; 99US-0136782.  
XX 01-JUN-1999; 99US-0137222.  
XX 03-JUN-1999; 99US-0137528.  
XX 04-JUN-1999; 99US-0137502.  
XX 07-JUN-1999; 99US-0137724.  
XX 08-JUN-1999; 99US-0138094.  
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XX 10-JUN-1999; 99US-0138847.  
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XX 18-JUN-1999; 99US-0139460.  
XX 18-JUN-1999; 99US-0139461.  
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XX 18-JUN-1999; 99US-0139750.  
XX 18-JUN-1999; 99US-0139753.  
XX 21-JUN-1999; 99US-0139817.  
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XX 23-JUN-1999; 99US-0140354.  
XX 24-JUN-1999; 99US-0140695.  
XX 28-JUN-1999; 99US-0140823.  
XX 29-JUN-1999; 99US-0140991.  
XX 30-JUN-1999; 99US-0141287.  
XX 01-JUL-1999; 99US-0141842.  
XX 01-JUL-1999; 99US-0142154.  
XX 02-JUL-1999; 99US-0142055.  
XX 06-JUL-1999; 99US-0142390.

PR 08-JUL-1999; 99US-0142803.  
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PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 18-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
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PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144684.  
PR 20-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145087.  
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PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
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PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
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PR 04-AUG-1999; 99US-0147204.  
PR 05-AUG-1999; 99US-0147302.  
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PR 06-AUG-1999; 99US-0147416.  
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PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148341.  
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PR 13-AUG-1999; 99US-0148684.  
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PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149902.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0153363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0154779.  
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PR 24-SEP-1999; 99US-0155659.  
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PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
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PR 08-OCT-1999; 99US-0158369.  
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PR 14-OCT-1999; 99US-0159331.  
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PR 21-OCT-1999; 99US-0160741.  
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PR 26-OCT-1999; 99US-0161361.  
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PR 28-OCT-1999; 99US-0161920.  
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PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 20.0%; Score 159; DB 21; Length 133;  
Best local similarity 32.3%; Pred. No. 2,66-10;  
Matches 43; Conservative 27; Mismatches 47; Indels 16; Gaps 6;

QY 9 IADCEITAFNDFRMSGNKANKTKFTIFKADNKKKEVVIDEV-SOEDEYEVFRSLKATKD 67  
Db 3 vsdecklkflekakrn---yflivfkidekagvmdk1gnpeelyedtrispede- 57  
QY 68 SKGNPAPRYAVYVEVDIGGEG-KRSKIVFISWVSDPTLMSMIVASTREBNKMLN- 125  
Db 58 -----cryavvd-ydfttpeqcqskifflawspdstsvrskmlyassksdrfkreld 109  
QY 126 IHTSIHADKGD 138  
Db 110 lqveldqatdpsem 122

RESULT 25  
AAG37448  
ID AAG37448 standard; Protein; 133 AA.  
XX AAG37448;  
XX 18-OCT-2000 (first entry)  
XX Arabidopsis thaliana protein fragment SEQ ID NO: 46047.  
XX DE  
XX Protein identification; signal transduction pathway; metabolic pathway;  
XX hybridisation assay; genetic mapping; gene expression control; promoter;  
XX termination sequence.  
XX Arabidopsis thaliana.  
XX OS  
XX EP1033405-A2.  
XX PN  
XX

PD 06-SEP-2000.  
XX  
XX 25-FEB-2000; 2000EP-0301439.  
PR 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
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PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
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PR 23-APR-1999; 99US-0130510.  
PR 28-APR-1999; 99US-0130891.  
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PR 07-MAY-1999; 99US-0132487.  
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PR 22-JUN-1999; 99US-0139899.  
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PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
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PR 04-AUG-1999; 99US-0147204.  
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PR 31-AUG-1999; 99US-0151430.  
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PR 10-SEP-1999; 99US-0153070.  
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PR 22-SEP-1999; 99US-0155139.

PR	23-SEP-1999;	99US-0135486.
PR	24-SEP-1999;	99US-0135659.
PR	28-SEP-1999;	99US-0156458.
PR	29-SEP-1999;	99US-0156596.
PR	04-OCT-1999;	99US-0157117.
PR	05-OCT-1999;	99US-0157753.
PR	06-OCT-1999;	99US-0157865.
PR	07-OCT-1999;	99US-0158029.
PR	08-OCT-1999;	99US-0158332.
PR	12-OCT-1999;	99US-0158369.
PR	13-OCT-1999;	99US-0159283.
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KM	termination sequence.
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OY	62	LEATKDSKGNPAPRAVYDVEYDLOGGEG-KRSKIVFISWPSDTPLTMSWIASTRENL	19.88;	Score 158;	DB 21;		
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OY	121	KNALN-IHTSIHADPKDIE	19.88;	Score 158;	DB 21;		
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XX AAG15708;

XX 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 16067.

XX Protein identification; signal transduction pathway; metabolic pathway;  
XX hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.

XX OS Arabidopsis thaliana.  
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XX PD 06-SEP-2000.  
XX PF 25-FEB-2000; 2000EP-0301439.  
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DB 97 lpade-----cryafld-fdfvsssegvpsrllffvawspdarlvrrskmlyassskdfr 147  
QY 121 KNALN-IHTSIHADKGDIE 139  
DB 148 krelgldqvelqatdptemd 167

Search completed: January 29, 2002, 18:16:44  
Job time: 3533 sec

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ACCESSION	AA788342
VERSION	AA788342.1
KEYWORDS	GI:2848573
SOURCE	EST.
ORGANISM	Emericella nidulans.
	Emericella nidulans.
	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
	Eurotiales; Trichocomaceae; Emericella.
REFERENCE	1 (Bases 1 to 474)
AUTHORS	Kudper, D., Gray, J., Hausner, J., Lai, H., Martin, W., Aramayo, R., Prade, R., and Roe, B.
TITLE	An Aspergillus nidulans EST Database
JOURNAL	Unpublished (1998)
COMMENT	Other ESTs: r7c08a1.f1
	Submitted by: Bruce A. Roe, University of Oklahoma, broe@ou.edu

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DEFINITION	AI211646 469 bp mRNA EST 19-OCT-1998
	g0f05a1.f1 Aspergillus nidulans 24hr asexual developmental and
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ACCESSION	AI211646	
VERSION	AI211646.1	GI:3773588
KEYWORDS	EST.	
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ORGANISM	<i>Emericella nidulans</i>	
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REFERENCE	1 (bases 1 to 403)
AUTHORS	Kupfer, D., Gray, J., Hausner, J., Lal, H., Martin, W., Aramayo, R., Prade, R., and Roe, B.
TITLE	An Aspergillus nidulans EST Database
JOURNAL	Unpublished (1998)
COMMENT	Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu Department of Chemistry and Biochemistry, University of Oklahoma

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FEATURES
  source      Email: broee@u.edu
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              'Seq primer: M13-20
              High quality sequence stop: 417.
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                1..469
                /organism="Emericella nidulans"

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developmental and vegetative cDNA lambda zap library"
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/vector="Vector: Bluescript SK-; Site_1: EcoRI; Site_2:
XhoI; 5' end of cDNA cloned into EcoRI site of bluescript
3' end of cDNA cloned into XhoI site of bluescript"
BASE COUNT
128 a 115 c 115 g 111 t
ORIGIN

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Qy	398	acgcagaagcgacacttagtgcgaagacttctgcgcgaagccagcggtgtgaagcc	456	
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 end of cDNA cloned into EcoRI site of pBluescript"

BASE COUNT  
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 BE517626  
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REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han  
 , P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Nausch, C.J.,  
 Seaton, C.L. and Tong, J.C.  
 The structure and function of the expressed portion of the wheat  
 genomes - Vernalized crown cDNA library  
 Unpublished (2000)  
 Contact: Olin Anderson  
 US Department of Agriculture, Agriculture Research Service, Pacific  
 West Area, Western Regional Research Center  
 800 Buchanan Street, Albany, CA 94710, USA  
 Tel: 5105595773  
 Fax: 5105595818  
 Email: oanderson@wr.usda.gov  
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 Seq primer: StrataGene SK primer.

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 Site\_1: EcoRI; Site\_2: XhoI; Seeds were germinated and  
 grown at 4 C for 5 weeks. The tissue, total RNA, and  
 poly(A) RNA were prepared. A cDNA library was made, and  
 the cDNA clones were in vivo excised to give pBluescript  
 phagemids in the T3 clone lab (Choi, Close, Fenton) at  
 the University of California, Riverside Plasmid DNA  
 preparations and DNA sequencing were performed in the OD  
 Anderson lab (all other authors)."

BASE COUNT  
 ORIGIN

99 a 168 c 186 g 95 t  
 10.6%; Score 49.2; DB 10; Length 548;  
 Query Match 50.7%; Pred. No. 0.0069; Indels 3; Gaps 1;  
 Best Local Similarity 0; Mismatches 138;

Matches 145; Conservative 0; Mismatches 138; Indels 3; Gaps 1;  
 93 gtccattatctcaagtcgcgcgatacaagaagaggtgtcatcgacgaagt---ctc 149  
 81 GTTCTGTGTTGATCAAGATGACGACGCGCTGACAGAGTGTGTGACAAAGTGGCGG 209  
 150 gcaagaagagagactacagaggtcttcgtagagctcgaggtctacaaagatagcaagg 209  
 141 CCGCGACGCGGCTTGCAGACGACGCGGCGGCACTCCCGGACGACTGCCGTACGC 200  
 210 taatccgctcctcgatgagctagatcagatcgagtagatcgtggtggtgaagg 269  
 201 CGTCTACGACCTTGAAGCTTACCGTGGGAGCGCCAAAGCGCGGAGGAGG 260  
 270 aaagagaagagatgtttcatctcctgtgttcctcagacacactactctgtgttc 329  
 261 GCCCGCAGCAAGATCTTCTCATCTCTGTCGCGCGGAGTCCGAGGAGGAAGACAA 320  
 330 catgattcagccagacacagcgaggaacttgaagaagcgtctcaac 375  
 321 GATGATCTACGCGAGCTCCACAGAGGGGTTCAAGAAAGAGCTGAC 366

RESULT 16  
 T36621/c 399 bp mRNA EST 11-JAN-1995  
 LOCUS EST101589 S. cerevisiae strain X2180-1A Saccharomyces cerevisiae  
 DEFINITION cDNA 3' end, mRNA sequence.  
 T36621  
 T36621.1 GI:620438  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 EST.  
 baker's yeast.  
 Saccharomyces cerevisiae  
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 Saccharomycetales; Saccharomycetaceae; Saccharomyces.

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 Weinstein, K.  
 Saccharomyces cerevisiae cDNAs  
 Unpublished (1995)  
 Other ESTs: TC295  
 Contact: Weinstein, K. and Venter, J.C.  
 The Institute for Genomic Research  
 932 Clopper Rd, Galtersburg, MD 20878  
 Tel: 3018699056  
 Fax: 3018699423  
 Email: tdbinfo@tdb.tigr.org  
 (tdbinfo@tdb.tigr.org)  
 Seq primer: M13-21.  
 Location/Qualifiers  
 1..399

FEATURES  
 source  
 1..399



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/organism="Saccharomyces cerevisiae"
/strain="X2180-1A"
/db_xref="taxon:4932"
/clone_lib="S. cerevisiae strain X2180-1A"
/notes="Vector: pBluescript SK-, Site_1: EcoRI, Site_2:
XhoI"

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/strain="X2180-1A"
/db xref="taxon:4932"
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7004:110973 -1277-00/

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/clone_lib="5. cerevisiae strain X2180-1A"
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/note="Vector: BLUEScript SK-: Site 1: ECORT: Site 2:

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“Xhoi”

BASE COUNT	128 a	71 c	68 g	126 t	6 others
ORIGIN					

ORIGIN

Query Match	Score	DB	Length
10.38;	48;	11;	399;
66.58;	48;	11;	399;
66.58;	48;	11;	399;

BEST LOCAL SIMILARITY 30.38; PRED. NO. 0.013;

Matches 87; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 222 tcgttatgcagtcctacgatatgtcgaatacgaatctcgttgagcgttgaggaagaagcaaa 281

100

QY 282 gatgttttcattctcctggttcctcagacacacctactctgtggtccatgatctacgc 341

\_\_\_\_\_

QY 342 cagcacacgagagaacttgaagaacgctctcaac 375

\_\_\_\_\_

201 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098 1099 1100 1101 1102 1103 1104 1105 1106 1107 1108 1109 1110 1111 1112 1113 1114 1115 1116 1117 1118 1119 1120 1121 1122 1123 1124 1125 1126 1127 1128 1129 1130 1131 1132 1133 1134 1135 1136 1137 1138 1139 1140 1141 1142 1143 1144 1145 1146 1147 1148 1149 1150 1151 1152 1153 1154 1155 1156 1157 1158 1159 1160 1161 1162 1163 1164 1165 1166 1167 1168 1169 1170 1171 1172 1173 1174 1175 1176 1177 1178 1179 1180 1181 1182 1183 1184 1185

## RESULT 17

REC'D 11  
AA001779/c

AA30110/C

LOCUS	AA901778	614 bp	mRNA
-------	----------	--------	------

**DEFINITION** NCM4B4T7 Mycelial Neurospora crassa

audience

sequence.  
14001770

RESULT	19
AWA01189	
Locus	392 bp mRNA EST
Definition	Landidigest35leat L.digitata gametophyte Lambda ZapII Lamnaria Laminalarria laminalaris 26S ribosomal protein S8, mRNA sequence
	07-FEB-2000

ACCESSION	AW401189.1	GI:6919679
VERSION	AW401189.1	
KEYWORDS	EST.	
SOURCE	Laminaria digitata.	
ORGANISM	Laminaria digitata	
	Phaeophyceae; Laminariales; Laminariaceae	

REFERENCE AUTHORS TITLE	1 (bases 1 to 3942) Creilneau, F., Roscoe, T., Kaas, R., Kloareg, B. and Boyen, C. Characterisation of complementary DNAs from the Expressed Tag analysis of life cycle stages of <i>Laminaria digitata</i> (Phaeophyceae)
JOURNAL COMMENT	unpublished (2000) Contact: Boyen C Centre d'Etudes Oceanologique et de Biologie Marine

**JOURNAL  
COMMENT**

unpublished (2000),  
Contact: Boyen C  
Centre d'Etudes Oceanologique et de Biologie Marine  
CNRS-LPR9042, Université P & M. Curie  
BP74, F-29682, Roscoff cedex, France  
Tel: 3 3 2 98 29 23 32  
Fax: 33 2 98 29 23 24  
Email: esteb-toscoff@ifremer.fr

FEATURES	source
Location/Qualities	1. .392
	/organism="Ramularia digitata"

ORIGIN	BASE COUNT
96 a	125 c
54 t	117 g

Query Match	9.24;	Score 43;	DB 10;	Length 392;
Best local Similarity	51.98;	Pred. No. 0.29;		
Matches	97;	Mismatches	90;	Indels 0;
				Gaps 0

QY	70	ggcaacaagggccaacaagaccgaatcatatcttcaagatgcgcgataacaagaagagag	129
Db	195	gcttcaaacagccgcagcaaacgagacttgcgcgaccacaagacccttgtttaagaaagccatc	254
QY	130	gtgtcatatcgacagagrtctcgcaagaagagactacagagtcttccttagagaggtcgaag	189
Db	255	gtgtgattcgacggccaccctttcaacatgcttggtagcaaacacattacggacgctgtc	314
QY	190	gtccacaagatagaagaaggtatcccgctccctcgttatcgagcttcaagatgtcgtatac	249
Db	315	ggatattcaagaaggcagaagatgcgcgcccttaaggccgagagagatccgtgcacaagtcg	374
QY	250	gattctcg	256
Db	375	gaccacg	381

	RESULT	20		
LOCUS	AW788192			
DEFINITION	C00264-R Lambda Zap <sup>+</sup> Stratagene Blumeria graminis f. sp. hordei CDNA clone C00264 similar to cofflin mRNA sequence.	382 bp	mRNA	EST 01-MAY-2001
ACCESSION	AW788192			
VERSION	AW788192.1	GI:13899789		
KEYWORDS	EST.			
SOURCE	Blumeria graminis f. sp. hordei.			
ORGANISM	Blumeria graminis f. sp. hordei Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;			

REFERENCE	TITLE	JOURNAL	COMMENT
1 (bases 1 to 382)	Gene identification in the fungal pathogen <i>Blumeria graminis</i> by expressed sequence tag analysis	Unpublished (2000)	Department of Yeast Genetics Carlsberg Laboratory 10 GI, Carlsbergvej, DK-2500, Copenhagen, Denmark Tel: 45 3327 5230 Fax: 45 3327 4766 Email: swr@crc.dk
2 (bases 1 to 382)	High quality sequence stop: 382		

FEATURES	source	Location/Qualities
1. .382		<i>Blumetia graminis</i> f. sp. <i>hordel</i>
/organism="Blumetia graminis f. sp. <i>hordel</i> "		
/db_xref="xref:62688"		
/clone="CO264"		
/clone_lib="Iambda zap, Stratsagene"		
/cell_type="confidia"		
/cell_host="hordem vulgare"		
BASE COUNT	130 a	81 c 76 g 95 t
ORIGIN		

9 1%: Score 42.4; DB 10; Length 382;

[illegible]

Db 188 AGAATTAATTTGTTCTCGCATGAGCCCATGACCTGGGIGIIMGCCAATTTT

OY 334 atctacgcacgacaggaagactgaagaa 365  
 DB 248 GTGTACGCTTCCTCCAGGCTTCACTCAAGAA 279

RESULT 21  
 LOCUS BH023930/c 510 bp DNA GSS 11-JUL-2001  
 DEFINITION 11 H. polymorpha DLI expression library Pichia angusta genomic, DNA  
 ACCESSION BH023930  
 VERSION BH023930  
 KEYWORDS GSS.  
 SOURCE Pichia angusta.  
 ORGANISM Pichia angusta.  
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 Saccharomycetales; Saccharomycetaceae; Pichia.

REFERENCE 1 (bases 1 to 510)  
 Agaphonov, M.O., Deev, A.V., Klim, S.-Y., Sohn, J.-H., Choi, E.-S. and Ter-Avanesyan, M.D.  
 Novel Reporter and Strategy for the Isolation and Functional Characterization of Transcriptionally Active Sequences in the Methylophilic Yeast Hansenula Polymorpha  
 Unpublished (2001)  
 CONTACT: Michael O. Agaphonov  
 Institute of Experimental Cardiology, Cardiology Research Center  
 3rd Cherepkovskaya Str. 15A, Moscow 121552, Russia  
 Tel: (095)4146734  
 Fax: (095)4146699  
 Email: aga@cardio.ru

H. polymorpha DLI genomic sequence homologous to the S. cerevisiae COR1 gene (complementary strand). Translation start is at 347 residue. Bases 344-294 and 282-236 correspond to introns.  
 Seq primer: gctgtacacctttatgc  
 Class: shotgun.

#### FEATURES

source  
 1..510  
 /organism="Pichia angusta"  
 /strain="H. polymorpha DL-1 leu2 mutant DLI-L"  
 /db\_xref="taxon:4905"  
 /clone\_lib="H. polymorpha DLI expression library"  
 /note="Vector: pKE32; Site 1: XhoI 2 bp filled-in; ATCC26012; 2-5 kb fraction of DNA fragments obtained by partial digestion of H. polymorpha DL-1 chromosomal DNA with Sau3A was ligated with XhoI-digested pKE32 vector. Two bp of the cohesive DNA ends were preliminary filled-in with Klenow enzyme. The XhoI site located upstream to the sequence encoding B. subtilis CMCase (D01057). Besides the reporter sequence encoding the CMCase, the vector bears the LEU2 gene and the fragment of 2um DNA of S. cerevisiae, that allows its stable autonomous maintenance in H. polymorpha CBS4732 cells."  
 BASE COUNT 113 a 122 c 126 g 149 t  
 ORIGIN

Query Match 9.0%; Score 42; DB 13; Length 510;  
 Best Local Similarity 55.8%; Pred. No. 0.57;  
 Matches 115; Conservative 0; Mismatches 70; Indels 21; Gaps 1;

OY 79 gccacaagacgaagtattatctcaagatgccgataacaagaagagtgatc 138  
 DB 186 GGCAAGAAAGTTCAAGTCATCATCTACAAAGCTGACGCAAAACGAGATCCTGTC 127  
 OY 139 gacgagctctgcagagagagagactagaggtcttcgtagcaggtcgcaggtacaa 198  
 DB 126 GACTTCACGCTCACAGAGAGAGCCCTACGACGCTTCTGTC----- 86  
 OY 199 gatagcaaggtaatccgctctcgtatgcagatcagatcagatcagatcgt 258  
 DB 87 GAGGACCTGCTGAAGAACGACTGATGATACGCGCTCTACGACTTGAGACAGGTGCGC 28

OY 259 ggcggtgaggaagaagaagaagat 284  
 DB 27 CAGGCGCAGCGCAGAGAAACAAGAT 2

RESULT 22  
 LOCUS AW710759/c 420 bp mRNA EST 25-APR-2000  
 DEFINITION e5h09ne.r1 Neurospora crassa evenling cDNA library Neurospora crassa  
 ACCESSION AW710759  
 VERSION AW710759  
 KEYWORDS EST.  
 SOURCE Neurospora crassa.  
 ORGANISM Neurospora crassa.  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Sordariiales; Sordariaceae; Neurospora.

REFERENCE 1 (bases 1 to 420)  
 Zhu, H., Lai, H., Kupfer, D., Dunlap, J.C. and Roe, B.A.  
 Two Neurospora crassa EST Databases  
 Unpublished (1998)  
 Other-ESTs: e5h09ne.r1  
 Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu  
 Department of Chemistry and Biochemistry  
 Advanced Center for Genome Technology, University of Oklahoma  
 620 Parrington Oval, Norman, OK 73019, USA  
 Tel: 405 325 4912  
 Fax: 405 325 7762  
 Email: broe@ou.edu

We anticipate the future release of the cDNA clones to the Fungal Genetics Stock Center  
 Seq primer: Universal Reverse Primer  
 High quality sequence stop: 274.

#### FEATURES

source  
 1..420  
 /organism="Neurospora crassa"  
 /strain="Strain 30-7 (bd; A)"  
 /db\_xref="taxon:5141"  
 /clone\_lib="e5h09ne"  
 /clone\_lib="Neurospora crassa evenling cDNA library"  
 /tissue\_type="tissue harvested following 22hr growth in dark"  
 /note="Vector: pBluescript SK-, Site 1: XbaI; Site 2: EcoRI; See: Bell-Petersen, D., et al. PNAS 93:13096,1996. 5' end of cDNA cloned into XbaI site of pBluescript; 3' end of cDNA cloned into EcoRI site of pBluescript"  
 BASE COUNT 105 a 107 c 100 g 108 t  
 ORIGIN

Query Match 8.9%; Score 41.6; DB 10; Length 420;  
 Best Local Similarity 52.8%; Pred. No. 0.7;  
 Matches 114; Conservative 0; Mismatches 99; Indels 3; Gaps 1;

OY 245 agtacgactcgtgtggtggtgaggaagaagaagatgtttcttcctctggtgc 304  
 DB 420 AGTACAAGCTTGGCTGTGCGGAGGTTCCCGCAACAAGTACCTTTATTCGCTGCTCC 361  
 OY 305 cctcgacacacacctctctgtgttcacatctacgcagcacagggagaaactgaaga 364  
 DB 360 CCGATGATGCTGGCATCAAGTCCAAAGATGCTTACGCTCTTCCAAAGAGGCCCTCAACG 301  
 OY 365 acgctctaac--atcacacctccatccacgctgcagacagagcgagacattggtga 421  
 DB 300 GCTCTCTACGCGATTCGCTGTCGAGCTCCAGGCCAACAGCAGCAGCAGCATCATGACTAG 241  
 OY 422 agacgtctctggtgcagagcgaggtgtgtaaggcg 457  
 DB 240 AACAGATTATCAAGACCGTACGACAGGATCTGCGC 205

RESULT 23  
 BF728099

REFERENCE		1 (bases 1 to 445)	
AUTHORS	Malbot,V.		
TITLE	Maize ESTs from various cDNA libraries sequenced at Stanford University		
JOURNAL COMMENT	Unpublished (1999) Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Plate: 485041 row: D column: 06. Location/Qualifiers		
FEATURES	source	1..445 /organism="Zea mays" /cultivar="B73" /db_xref="taxon:4577" /clone_id="486 - Leaf primordia cDNA library from Hake lab" /tissue-type="leaf primordia" /dev_stage="p7-pil leaf" /lab_host="E.coli XL1-Blue MFR" /note="Organ: shoot; Vector: lambda zap; Hake lab cDNA library"	
BASE COUNT	83 a     125 c     110 g     127 t		
ORIGIN			
Query Match	8.9%; Score 41.4;	DB 10;	Length 445;
Best Local Similarity	58.5%;	Pred.No. 0.8;	51; Indels 0; Gaps 0;
Matches 72:	Conservative		
OY	62 gcacgagcggaacaaggcccaagaaccaagtcatatcttcgaagatgcggatacca	121	
Db	293 GGATGGGAGGAACCAACAACCATCAGAAGCTCAAGTCCGCAGATCGAACAACC	234	
OY	122 agaaggaaagttgtcattcgacgaagtgctcgcgaagaagaagactcgaagtcctccgtga	181	
Db	233 TCCGGGTGTCATTGATCATCAAGGGGCCGTCGCAGGGAA GCCCGGAACCTCCTCCGATA	174	
OY	182 gcc 184    Db	173 CGC 171	
RESULT 25			
AM330907	451 bp mRNA	EST	31-JAN-2000
LOCUS	707023f02.x3 707 - Mixed adult tissues from Walbot Lab (SK) Zea		
DEFINITION	mays cDNA, mRNA sequence.		
ACCESSION	AM330907		
VERSION	AM330907.1 GI:6827264		
KEYWORDS	EST.		
SOURCE	Zea mays.		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC Clade; Panicoideae; Andropogoneae; Zea.		
REFERENCE	1 (bases 1 to 451)		
AUTHORS	Walbot,V.		
TITLE	Maize ESTs from various cDNA libraries sequenced at Stanford University		
JOURNAL COMMENT	Unpublished (1999) Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Plate: 707023 row: F column: 02. Location/Qualifiers		
FEATURES			

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source
1. .451
/organism="Zea mays"
/cultivar="W23"
/db_xref="taxon:4577"
/clone_id="707 - Mixed adult tissues from Walbot lab (SK
)"
/tissue_type="tassel, kernel, silk, husk, root, leaf"
/dev_stage="adult"
/lab_host="DH10B"
/Note="Organ: tassel, kernel, silk, husk, root, leaf;
Vector: pGAD10; Site: 1: EcoRI; cDNA library from fully
differentiated maize tissues from an active Mutator
plant. Tissue ratio is 4/2/1/1/1 (tassel, kernel, silk,
husk, root, leaf). Unidirectionally cloned."

BASE COUNT      138 a      100 c      120 g      93 t
ORIGIN

Query Match      8.9%  Score 41.4; DB 10; Length 451;
Best Local Similarity 58.5%  Pred. No. 0.8;
Matches 72; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Oy 62 gcatgagcgacacaaaggccaagaccagatcatctctcaagatcgccgataaca 121
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 73 GGATGGGAGGACCAAGACCAAGATCAGAGAGCTCAAGATCGACAAACAACC 132

Oy 122 agaaggaaggtgttcacgcagaggtctcgcagaagaagactcagaggtcttcgtagca 181
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 133 TCCGGGTGCTCATGATCAAGGGGCCGTGCCAGGAGACCCGGGAACTCTCCGCATATA 192

Oy 182 ggc 184
    ||
Db 193 CGC 195

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RESULT 26
BG842914 550 bp mRNA EST 29-MAY-2001
LOCUS BG842914.1
DEFINITION MEST41-E07.T3 ISUM4-TN Zea mays cDNA clone MEST41-E07.3, mRNA
sequence.
ACCESSION BG842914
VERSION BG842914.2 GI:14244976
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.
REFERENCE Eukaryotes: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
TITLE clade: Panicoideae; Andropogoneae; Zea.
JOURNAL 1 (bases 1 to 550)
COMMENT Qiu,F., Cui,F., Guo,L., Ashlock,D.A., Wen,T.J. and Schnable,P.S.
Unpublished Sequence Tags from B73 Maize Seedlings and Silks
On May 25, 2001 this sequence version replaced gi:14209236.
CONTACT: Patrick S. Schnable
Schnable Laboratory
Iowa State University
G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu
PCR Primers
FORWARD: T7-1 (AA TAC GAC TCA CTA TNG)
BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).
Location/Qualifiers
1. .550
/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone_id="MEST41-E07"
/clone_1db="ISUM4-TN"
/tissue_type="Seedling and silk"
/lab_host="DH10B"

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FEATURES
source
1. .550
/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone_id="MEST41-E07"
/clone_1db="ISUM4-TN"
/tissue_type="Seedling and silk"
/lab_host="DH10B"

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/Note="Vector: pRT3PAC; Site: 1: EcoRI; Site: 2: NotI;
ds-cDNA molecules were generated as follows: First-strand
cDNA was prepared from oligo-dT selected mRNA by priming
with a NotI oligo-dT primer (5'
AAGCGAAGAAATTCGCGCCGCGCAGGAAATTTTTTTTTTTTTT). The
resulting DNA:RNA hybrid was treated with RNase H and used
as a template for DNA Pol-catalyzed second strand
synthesis. After the addition of EcoRI adaptors, the
ds-cDNAs were digested with NotI and size-selected. The
resulting molecules were directionally cloned into the
EcoRI and NotI sites of the pRT3PAC vector. The library
then went through one round of normalization to Cot value
of 5 based on the methods of Marcelo Bento Soares (Genome
Research 6: 791-806, 1996)."

BASE COUNT      100 a      153 c      156 g      141 t
ORIGIN

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Query Match      8.9%  Score 41.4; DB 11; Length 550;
Best Local Similarity 58.5%  Pred. No. 0.84;
Matches 72; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

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Db 229 TCCGGGTGCTCATGATCAAGGGGCCGTGCCAGGAGACCCGGGAACTCTCCGCATATA 170

Oy 182 ggc 184
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Db 169 CGC 167

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RESULT 27
AUI76493 448 bp mRNA EST 21-MAR-2001
LOCUS AUI76493
DEFINITION AUI76493 Rice immature leaf including apical meristem (under long
day condition) Oryza sativa cDNA clone E51253, mRNA sequence.
ACCESSION AUI76493
VERSION AUI76493.1 GI:13422855
KEYWORDS EST.
SOURCE Oryza sativa.
ORGANISM Oryza sativa.
REFERENCE Eukaryotes: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
TITLE Euhartoidae; Oryzaceae; Oryza.
JOURNAL 1 (bases 1 to 448)
COMMENT Sasaki,T. and Yamamoto,K.
Rice cDNA from immature leaf including apical meristem (2001)
Unpublished (2001)
CONTACT: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@abrr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
PROJECT = 'RGP'.
E51253..97A.
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/cultivar="Nipponbare"
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/clone_id="E51253"
/clone_1db="Rice immature leaf including apical meristem
(under long day condition)"
/dev_stage="Immature leaf including apical meristem (under
long day condition)"

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/cultivar="Nipponbare"
/db_xref="taxon:4530"
/clone_id="E51253"
/clone_1db="Rice immature leaf including apical meristem
(under long day condition)"
/dev_stage="Immature leaf including apical meristem (under
long day condition)"
BASE COUNT      114 a      103 c      149 g      82 t
ORIGIN

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 29, 2002, 16:12:31 ; Search time 88.13 Seconds  
(without alignments)  
1194.965 Million cell updates/sec

Title: US-09-722-838-1

Perfect score: 465

Sequence: 1 atggcgcgcgcacccgcgtgt.....gtgtaagccgtaataag 465

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113236999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents.NA:\*  
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2: /cgn2\_6/prodata/2/lna/5B\_COMB.seq:\*  
3: /cgn2\_6/prodata/2/lna/6A\_COMB.seq:\*  
4: /cgn2\_6/prodata/2/lna/6B\_COMB.seq:\*  
5: /cgn2\_6/prodata/2/lna/PCFUS\_COMB.seq:\*  
6: /cgn2\_6/prodata/2/lna/Backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39.4	8.5	5515	4	US-09-398-193-98 Sequence 98, Appl
2	36.2	7.8	1545	1	US-08-759-579-1 Sequence 1, Appl
3	36.2	7.8	1583	2	US-08-532-795-1 Sequence 1, Appl
4	36.2	7.8	1726	2	US-08-532-795-22 Sequence 22, Appl
5	36.2	7.8	1728	2	US-08-532-795-24 Sequence 24, Appl
6	36.2	7.8	1729	2	US-08-532-795-18 Sequence 18, Appl
7	36.2	7.8	1731	2	US-08-532-795-28 Sequence 28, Appl
8	36.2	7.8	1732	2	US-08-532-795-20 Sequence 20, Appl
9	36.2	7.8	1741	2	US-08-532-795-26 Sequence 26, Appl
10	36.2	7.8	1845	1	US-08-014-531-1 Sequence 1, Appl
11	36.2	7.8	1845	1	US-08-262-338A-1 Sequence 1, Appl
12	36.2	7.8	1845	1	US-08-460-114A-1 Sequence 1, Appl
13	35.2	7.6	1709	2	US-09-010-398-2 Sequence 2, Appl
14	35.2	7.6	1709	4	US-09-366-260-2 Sequence 2, Appl
15	35.2	7.6	1709	4	US-09-153-804-11 Sequence 11, Appl
16	34.6	7.4	462	1	US-08-450-945-66 Sequence 66, Appl
17	34.6	7.4	462	1	US-08-976-161-66 Sequence 66, Appl
18	34.6	7.4	2057	4	US-08-450-945-57 Sequence 57, Appl
19	34.6	7.4	2057	4	US-08-976-161-57 Sequence 57, Appl
20	34	7.3	1588	3	US-08-389-564B-16 Sequence 16, Appl
21	34	7.3	1588	3	US-08-466-047B-16 Sequence 16, Appl
22	33.8	7.3	1386	2	US-08-658-665-53 Sequence 53, Appl
23	33.8	7.3	1386	2	US-08-796-101-17 Sequence 17, Appl
24	33.8	7.3	1386	4	US-09-085-273-53 Sequence 53, Appl
25	33.8	7.3	1476	4	US-08-658-665-50 Sequence 50, Appl
26	33.8	7.3	1476	4	US-08-796-101-14 Sequence 14, Appl
27	33.8	7.3	1476	4	US-09-085-273-50 Sequence 50, Appl

28	33.8	7.3	1740	4	US-08-796-101-50 Sequence 50, Appl
29	33.8	7.3	1975	2	US-08-658-665-51 Sequence 51, Appl
30	33.8	7.3	1975	4	US-08-796-101-15 Sequence 15, Appl
31	33.8	7.3	1975	4	US-09-085-273-51 Sequence 51, Appl
32	33.8	7.3	3409	2	US-08-658-665-54 Sequence 54, Appl
33	33.8	7.3	3409	4	US-08-796-101-18 Sequence 18, Appl
34	33.8	7.3	3409	4	US-09-085-273-54 Sequence 54, Appl
35	33.8	7.3	3499	2	US-08-658-665-52 Sequence 52, Appl
36	33.8	7.3	3499	4	US-08-796-101-16 Sequence 16, Appl
37	33.8	7.3	3499	4	US-09-085-273-52 Sequence 52, Appl
38	32.8	7.1	1341	2	US-08-945-848-7 Sequence 7, Appl
39	32.8	7.1	2363	2	US-08-945-848-6 Sequence 6, Appl
40	32.8	7.1	3231	5	US-08-074-121-4 Sequence 4, Appl
41	32.8	7.1	3231	5	PCT-US94-06447-4 Sequence 4, Appl
42	32.4	7.0	2952	4	US-09-318-794A-4 Sequence 4, Appl
43	32.4	7.0	3784	1	US-07-623-033-1 Sequence 1, Appl
44	32.2	6.9	2225	1	US-08-450-945-56 Sequence 56, Appl
45	32.2	6.9	2225	4	US-08-976-161-56 Sequence 56, Appl

## ALIGNMENTS

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RESULT 1
US-09-398-193-98
; Sequence 98, Application US/09398193
; Patent No. 6197581
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: Adenylate cyclase and uses therefor
; FILE REFERENCE: P24360-
; CURRENT APPLICATION NUMBER: US/09/398,193
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 5515
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (539)..(4600)
US-09-398-193-98
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Query Match 8.5%; Score 39.4; DB 4; Length 5515;  
Best Local Similarity 57.9%; Pred. No. 0.068;  
Matches 70; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

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QY 388 atccagcctcagcagcagcgagcagatgtggaagacttttcggccggcgcaagcgt 447
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Db 3749 tacgagaggaactcagcgagcgagcagagagtgctaccgggtcttccaagcgactcgc 3608
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QY 448 g 448

Db 3809 g 3809

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RESULT 2
US-08-759-579-1
; Sequence 1, Application US/08759579
; Patent No. 5798242
; GENERAL INFORMATION:
; APPLICANT: Kinaya, Fujishiro
; APPLICANT: Takayuki, Uwajima
; TITLE OF INVENTION: NOVEL CHOLESTEROL OXIDASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Antonelli, Terry, Stout & Kraus
```

CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIKAIIDO, MARMELESTEIN, MURRAY & ORAM LLP  
STREET: 655 Fifteenth Street, N. W., Suite 330 - G  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/532,795  
FILING DATE: 06-NOV-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P 43 14 793.3  
FILING DATE: 05-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P 43 42 012.5  
FILING DATE: 09-DEC-1993  
APPLICATION DATA: PCT/EP94/01394  
APPLICATION NUMBER: PCT/EP94/01394  
FILING DATE: 02-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: KLESNER, Sharon N.  
REGISTRATION NUMBER: 36,335  
REFERENCE/DOCKET NUMBER: P1614-5064  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/638-5000  
TELEFAX: 202/638-4810  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1683 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1683  
US-08-532-795-1

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Best Local Similarity 53.1%; Pred. No. 0.36; Mismatches 68; Indels 0; Gaps 0;
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Db      237 GCCCAACGTCGAGAAGGTGATCTCCGCCGACACGATGACGATCTGAACGGCATCACG 256

QY      171 ctccgtagcaggtctcgagctacc 195
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Db      297 GAACACGGCGGCCCGCGTGGCTAC 321

RESULT      4
US-08-532-795-22
: Sequence 22, Application US/08532795
: Patent No. 5916759
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: GENERAL INFORMATION:
: APPLICANT: JARSCH, Michael
: TITLE OF INVENTION: CHOLESTEROL OXIDASE FROM BREVIABACTERIUM
: TITLE OF INVENTION: STEROLICUM
: NUMBER OF SEQUENCES: 34
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: NIKAIIDO, MARNELESTELIN, MURRAY & ORAM LLP
:

```



COUNTRY: USA  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/532,795  
FILING DATE: 06-NOV-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P 43 14 793.3  
FILING DATE: 05-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P 43 42 012.5  
FILING DATE: 09-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP94/01394  
FILING DATE: 02-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: KLESNER, Sharon N.  
REGISTRATION NUMBER: 36,335  
REFERENCE/DOCKET NUMBER: P1614-5064  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/638-5000  
TELEFAX: 202/638-4810  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1729 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 17..1729  
US-08-532-795-18

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Matches 77; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 51 caacgatttcgcgatgagggcaacaagccacaagaagcaagttatattttcaagat 110  
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QY 171 ctccgtagcaggtctcgaggtacc 195  
DB 343 GAACACGGGGCGGCCCGGTGCTACC 367

RESULT 7  
US-08-532-795-28  
Sequence 28, Application US/08532795  
Patent No. 5916759  
GENERAL INFORMATION:  
APPLICANT: JARSCH, Michael  
TITLE OF INVENTION: CHOLESTEROL OXIDASE FROM BREVIABACTERIUM  
TITLE OF INVENTION: STEROLICUM  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIKAIKO, MARCELSTEIN, MURRAY & ORAM LLP  
STREET: 655 Fifteenth Street, N. W., Suite 330 - G  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-5701

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/532,795  
FILING DATE: 06-NOV-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P 43 14 793.3  
FILING DATE: 05-MAY-1993  
PRIOR APPLICATION DATA:  
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FILING DATE: 09-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP94/01394  
FILING DATE: 02-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: KLESNER, Sharon N.  
REGISTRATION NUMBER: 36,335  
REFERENCE/DOCKET NUMBER: P1614-5064  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/638-5000  
TELEFAX: 202/638-4810  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1731 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 25..1731  
US-08-532-795-28

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Matches 77; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

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QY 111 cgcgataacaagaagaggtgtcatcgagaggtctcgcaagaagaggaactaagagt 170  
DB 285 GGCACAGCTCAGAGAGGTGATCTCGCCGACACGATGACGATCTGAACGCGATCACGGT 344  
QY 171 ctccgtagcaggtctcgaggtacc 195  
DB 345 GAACACGGGGCGGCCCGGTGCTACC 369

RESULT 8  
US-08-532-795-20  
Sequence 20, Application US/08532795  
Patent No. 5916759  
GENERAL INFORMATION:  
APPLICANT: JARSCH, Michael  
TITLE OF INVENTION: CHOLESTEROL OXIDASE FROM BREVIABACTERIUM  
TITLE OF INVENTION: STEROLICUM  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIKAIKO, MARCELSTEIN, MURRAY & ORAM LLP  
STREET: 655 Fifteenth Street, N. W., Suite 330 - G  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/532,795
  FILING DATE: 06-NOV-1995
  CLASSIFICATION: 435
  PRIORITY APPLICATION DATA:
    APPLICATION NUMBER: DE P 43 14 793.3
    FILING DATE: 05-MAY-1993
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: DE P 43 42 012.5
    FILING DATE: 09-DEC-1993
  PRIORITY APPLICATION DATA:
    APPLICATION NUMBER: PCT/EP94/01394
    FILING DATE: 02-MAY-1994
  ATTORNEY/AGENT INFORMATION:
    NAME: KLESNER, Sharon N.
    REGISTRATION NUMBER: 36,335
    REFERENCE/DOCKET NUMBER: P1614-5064
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: 202/638-5000
      TELEFAX: 202/638-4810
    INFORMATION FOR SEQ ID NO: 20:
      SEQUENCE CHARACTERISTICS:
        LENGTH: 1732 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: single
        TOPOLOGY: linear
      FEATURE:
        NAME/KEY: CDS
        LOCATION: 20..1732
US-08-532-795-20

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Query Match 7.8%; Score 36.2; DB 2; Length 1732;

Best Local Similarity 53.1%; Pred. No. 0.36; Mismatches 68; Indels 0; Gaps 0;

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QY 111 cgcgataaacaagaagaggttgatcatcgacgaggtctcgcaagaagagctagaagt 170
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DB 286 GGCACAGCTGACAGAGTGATCTCGCCGACAGATGACGATCTGACGATCAGCGT 345
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DB 346 GAACACGGCGCGCGCGCTGCTACC 370

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RESULT 9

US-08-532-795-26

; Sequence 26, Application US/08532795

; Patent No. 5916759

; GENERAL INFORMATION:

; APPLICANT: JASCH, Michael

; TITLE OF INVENTION: CHOLESTEROL OXIDASE FROM BREVIACTERIUM

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIKAIKO, MARCELSTEIN, MURRAY & ORAM LLP

; STREET: 655 Fifteenth Street, N. W., Suite 330 - G

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20005-5701

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/532,795
  FILING DATE: 06-NOV-1995
  CLASSIFICATION: 435
  PRIORITY APPLICATION DATA:
    APPLICATION NUMBER: DE P 43 14 793.3
    FILING DATE: 05-MAY-1993
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: DE P 43 42 012.5
    FILING DATE: 09-DEC-1993
  PRIORITY APPLICATION DATA:
    APPLICATION NUMBER: PCT/EP94/01394
    FILING DATE: 02-MAY-1994
  ATTORNEY/AGENT INFORMATION:
    NAME: KLESNER, Sharon N.
    REGISTRATION NUMBER: 36,335
    REFERENCE/DOCKET NUMBER: P1614-5064
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: 202/638-5000
      TELEFAX: 202/638-4810
    INFORMATION FOR SEQ ID NO: 26:
      SEQUENCE CHARACTERISTICS:
        LENGTH: 1741 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: single
        TOPOLOGY: linear
      FEATURE:
        NAME/KEY: CDS
        LOCATION: 20..1741
US-08-532-795-26

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Query Match 7.8%; Score 36.2; DB 2; Length 1741;

Best Local Similarity 53.1%; Pred. No. 0.36; Mismatches 68; Indels 0; Gaps 0;

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Matches 77; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
QY 51 caacgaatttcgcgatgagcgcaacaagggcaacgaagtcattcttcaaat 110
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DB 235 CTACAGATGTCGGCGCGCGCGCGATGACAGCGGCTGACCGCTGAGAAAGG 294
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 111 cgcgataaacaagaagaggttgatcatcgacgaggtctcgcaagaagagctagaagt 170
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 295 GGCACAGCTGACAGAGTGATCTCGCCGACAGATGACGATCTGACGATCAGCGT 354
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QY 171 ctccgtacgagctcgagctacc 195
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DB 355 GAACACGGCGCGCGCGCTGCTACC 379

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RESULT 10

US-08-014-531-1

; Sequence 1, Application US/08014531

; Patent No. 5371005

; GENERAL INFORMATION:

; APPLICANT: Fujishiro, Kiya

; TITLE OF INVENTION: No. 5371005el Cholesterol Oxidase

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ANTONELLI, TERRY, STOUT AND KRAUS

; STREET: Suite 600, 1919 Pennsylvania Avenue, N.W.

; CITY: Washington, D.C.

; COUNTRY: U.S.A.

; ZIP: 20006

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk, 3.50inch, 800kb storage

; OPERATING SYSTEM: Macintosh 6.0.4

; SOFTWARE: HyperCard 1.2.2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/014,531

; FILING DATE: 19930208

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/798,660  
FILING DATE: 26-NOV-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/683,539  
FILING DATE: 10-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Terry, David T.  
REGISTRATION NUMBER: 20178  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-828-0300  
TELEFAX: 202-828-0380  
TELEX: 440280  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1845 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
ORIGINAL SOURCE: Brevibacterium sterolicum  
ORGANISM: ATCC21387  
STRAIN: ATCC21387  
US-08-014-531-1

Query Match 7.8%; Score 36.2; DB 1; Length 1845;  
Best Local Similarity 53.1%; Pred. No. 0.37; Indels 0; Gaps 0;  
Matches 77; Conservative 0; Mismatches 68

QY 51 caacgattccgtagagcgcaacaagaagccaaagttcattatcttcaagat 110  
DB 333 CTACAAAGATCGCGCCGCGCGGCGATGCAAGCGCTGACCCCTGAGAGG 392  
QY 111 cgcgataacaagaagaggtgtcatcgacgaggtctcgcaagaagagactagaggt 170  
DB 393 GGCACAGCTGAGAGGTGATCTCGCGCACGATGACGATCTGAACGCAATCAGGT 452  
QY 171 ctccgtagcagagctcgagctacc 195  
DB 453 GAACACGGGCGGCCCTGTGCTAC 477

RESULT 11  
US-08-262-338A-1  
Sequence 1, Application US/08262338A  
Patent No. 5602017  
GENERAL INFORMATION:  
APPLICANT: Fujishiro, Kinya  
APPLICANT: Uwajima, Takayuki  
TITLE OF INVENTION: NOVEL CHOLESTEROL OXIDASE  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ANTONELLI, TERRY, STOUT AND KRAUS  
STREET: Suite 1800, 1300 No. 5602017th Seventeenth Street  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22209  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/262,338A  
FILING DATE: 06/17/94  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/683,539  
FILING DATE: 10-APR-1991  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/798,660  
FILING DATE: 26-NOV-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/014,531  
FILING DATE: 8-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Terry, David T.  
REGISTRATION NUMBER: 20,178  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)312-6600  
TELEFAX: (703)312-6666  
TELEX: 248545  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1845 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM: Brevibacterium sterolicum  
STRAIN: ATCC 21387  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Unicellular organism  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY: genomic  
CLONE: pmh10  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY: express cholesterol oxidase II activity  
IDENTIFICATION METHOD:  
LOCATION:  
OTHER INFORMATION:  
US-08-262-338A-1

Query Match 7.8%; Score 36.2; DB 1; Length 1845;  
Best Local Similarity 53.1%; Pred. No. 0.37; Indels 0; Gaps 0;  
Matches 77; Conservative 0; Mismatches 68

QY 51 caacgattccgtagagcgcaacaagaagccaaagttcattatcttcaagat 110  
DB 333 CTACAAAGATCGCGCCGCGCGGCGATGCAAGCGCTGACCCCTGAGAGG 392  
QY 111 cgcgataacaagaagaggtgtcatcgacgaggtctcgcaagaagagactagaggt 170  
DB 393 GGCACAGCTGAGAGGTGATCTCGCGCACGATGACGATCTGAACGCAATCAGGT 452  
QY 171 ctccgtagcagagctcgagctacc 195  
DB 453 GAACACGGGCGGCCCTGTGCTAC 477

RESULT 12  
US-08-460-114A-1  
Sequence 1, Application US/08460114A  
Patent No. 5663560  
GENERAL INFORMATION:  
APPLICANT: Fujishiro, Kinya  
APPLICANT: Uwajima, Takayuki  
TITLE OF INVENTION: NOVEL CHOLESTEROL OXIDASE



```

1  APPLICANT: Julian Gordon
2  APPLICANT: Steven C. Hodges
3  APPLICANT: Michael R. Klass
4  APPLICANT: Jon D. Kratochvill
5  APPLICANT: Eric Russell
6  APPLICANT: Stephen D. Stroupe
7  TITLE OF INVENTION: Reagents and Methods Useful for Detecting Diseases of the Urin
8  TITLE OF INVENTION: Tract
9  TITLE OF INVENTION: 6180 US 01
10 FILE REFERENCE: 6180 US 01
11 CURRENT APPLICATION NUMBER: US/09/153,804
12 CURRENT FILING DATE: 1998-09-15
13 NUMBER OF SEQ ID NOS: 17
14 SOFTWARE: FASTSEQ for Windows Version 3.0
15 SEQ ID NO 11
16 LENGTH: 1709
17 TYPE: DNA
18 ORGANISM: Homo sapiens
19 US-09-153-804-11

```

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Query Match          7.6%; Score 35.2; DB 4; Length 1709;
Best Local Similarity 53.7%; Pred. No. 0.63; Mismatches 63; Indels 0; Gaps 0;
Matches 73; Conservative

OY      322 ctgtgctcatgatcctacgcgcagcacagcggaagaacttgaagacgctctcaatccac 381
        || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      548 ctccggagcaagatcatcattgaccacacatcgcataactcccggctcatccttgaaatcgac 607
        || | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY      382 accttcaccacagctcgcagcaagaaggcgacattgagtggaaacgtttctggccgaagcc 441
        | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      608 aatgcgaagctcgctctgcggagacattcagctcaaglatgaaatgacatgcgacctgtgcgc 667
        || | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY      442 agcggttgtaagcgccg 457
        || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      668 caggcgcttgtaggctg 683

RESULT 16
US-08-450-945-66/C
; Sequence 66, Application US/08450945
; Patent No. 5783383
GENERAL INFORMATION:
APPLICANT: Kondo, Kazuhiko
APPLICANT: Mocarski, Edward S., Jr.
TITLE OF INVENTION: LATENT TRANSCRIPTS AND PROMOTERS
TITLE OF INVENTION: OF CYTOMEGALOVIRUS
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,945
FILING DATE: 23-MAY-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles R.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8600-0157
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO.: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 462 base pairs

```



```

?      TYPE: nucleic acid
?      STRANDEDNESS: double
?      TOPOLOGY: linear
?      MOLECULE TYPE: cDNA to mRNA
?      HYPOTHETICAL: NO
?      ANTI-SENSE: NO
?      ORIGINAL SOURCE:
?      INDIVIDUAL ISOLATE: antisense ORF 2
?      FEATURE:
?      NAME/KEY: CDS
?      LOCATION: 1..462
?      OS:
?      OS-08-450-945-66

```

	Query Match	7.4%;	Score 34.6;	DB 1;	Length 462;
	Best Local Similarity	48.3%;	Pred. No. 0.64;		
	Matches	97;	Conservative	0;	Mismatches 104; Indels 0; Gaps 0;
QY	17	gtgtctctatcgacagatgagtgacattactgcattcaacgatttcgcgcatgagcgacaca	76		
Db	266	GTGACCCCTGTGCTTATACCTCTATTTCATGTTTATAGGCCGAGACCCGTTGACCA	207		
QY	77	agggcaacaagaaccaagctcattatctcaaatgcgcgcataacaagaagagtggttga	136		
Db	206	AGGCCACACACGTTCTCTGCAGACTATGTTGAGGAAGAGGTTAACTCAGCTGAGCTCG	147		
QY	137	tcgacagaggtctcgcaagaagagactacgaggtcttcgttagcaagtcgaggtctacca	196		
Db	146	GAGACCCCTGTTTCCAGATGTGGCCGGAAGATCCCTCAAACTTTTGAACAAGATGCCG	87		
QY	197	aggatagcaaggtgtaattcccg	217		
Db	86	AGGATTGCAACGACGAAACCCCG	66		

RESULT 17  
 US-08-976-161-66/c  
 Sequence 66, Application US/08976161  
 Patent No. 6194542  
 GENERAL INFORMATION:  
 APPLICANT: Kondo, Kazuhito  
 APPLICANT: MocarSKI, Edward S. Jr.  
 TITLE OF INVENTION: LATENT TRANSCRIPTS AND PROMOTERS  
 TITLE OF INVENTION: OF CYTOMEGALOVIRUS  
 NUMBER OF SEQUENCES: 75  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Dehlinger & Associates  
 STREET: 350 Cambridge Avenue, Suite 250  
 City: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94306  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/976,161  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/450,945  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Sholtz, Charles K.  
 REGISTRATION NUMBER: 38,615  
 REFERENCE/DOCKET NUMBER: 8600-0157  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 324-0880  
 TELEFAX: (415) 324-0960  
 INFORMATION FOR SEQ ID NO: 66:  
 SEQUENCE CHARACTERISTICS:

```

?      LENGTH: 462 base pairs
?
?      TYPE: nucleic acid
?
?      STRANDEDNESS: double
?
?      TOPOLOGY: linear
?
?      MOLECULE TYPE: cDNA to mRNA
?
?      HYPOTHETICAL: NO
?
?      ANTI-SENSE: NO
?
?      ORIGINAL SOURCE:
?
?      INDIVIDUAL ISOLATE: antisense ORF 2
?
?      FEATURE:
?
?      NAME/KEY: CDS
?      LOCATION: 1..462
?
US-08-976-161-66

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	Query Match	7.4%	Score 34.6	DB 4	Length 462
	Best Local Similarity	48.3%	Pred. No. 0.64		
	Matches	97	Conservative	0	Mismatches 104
					Indels 0
					Gaps 0
OY	17	gtctctctatcgagatgagtgatcattactgcatctcaagatttcgcgcatgagcggcaaca	76		
Db	266	GTGACCCCATGTGCTCTATGACTCTATTTCCTCAGTGTGTATGGCCCGAGAACCCGTGACCA	207		
OY	77	aggccacaacaagacaaagtctcatctatcttcctaagatgcgcgataacaagaagaggtgtgca	136		
Db	206	AGGCCACGACGCTTCCTGCGACTATAGTTGAGGAAGAGAGGTTAACATCAGCTGAGTCTGG	147		
OY	137	tcgaagaggtctcgcaagaagaagagactcgaagttcttcgttagcagagctcgagagctaacca	196		
Db	146	GAGACCCCGCTGTTCCAGATGTGGCCGGAAGATCCCTCAAACTTTTGAAACAAGTGACCG	87		
OY	197	aggatagcaagaaggtatctccc	217		
Db	86	AGGATTTCACAACGAGAACCCG	66		

RESULT 18  
 US-08-450-945-57/c  
 Sequence 57, Application US/08450945  
 Patent No. 5783383  
 GENERAL INFORMATION:  
 APPLICANT: Kondo, Kazuhiko  
 APPLICANT: Mocaraki, Edward S. Jr.  
 TITLE OF INVENTION: LATENT TRANSCRIPTS AND PROMOTERS  
 TITLE OF INVENTION: OF CYTOMEGALOVIRUS  
 NUMBER OF SEQUENCES: 75  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Dehlinger & Associates  
 STREET: 350 Cambridge Avenue, Suite 250  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94306  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/450,945  
 FILING DATE: 23-MAY-1995  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Sholtz, Charles K.  
 REGISTRATION NUMBER: 38,615  
 REFERENCE/DOCKET NUMBER: 8600-0157  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 324-0880  
 TELEFAX: (415) 324-0960  
 INFORMATION FOR SEQ. ID NO: 57:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2057 base pairs  
 TYPE: nucleic acid

```

?      TOPOLOGY: unknown
?      MOLECULE TYPE: CDNA to mRNA
?      HYPOTHETICAL: NO
?      ANTI-SENSE: YES
?      ORIGINAL SOURCE:
?      INDIVIDUAL ISOLATE: region of Ad169 strain HCMV (antisense)
?      INDIVIDUAL ISOLATE: containing antisense transcript ORFs
?      US-08-976-161-57
Query Match      7.4%; Score 34.6; DB 4; Length 2057;

```

[illegible][illegible]

RESULT 20  
US-08-389-564B-16  
; Sequence 16, Application US/08389564B  
; Patent No. 5983870  
; GENERAL INFORMATION:  
; APPLICANT: Nakari, Tiina H.  
; APPLICANT: Onnela, Maija-Leena  
; APPLICANT: Iim u, Marja H.  
; APPLICANT: Penttil, Merja E.  
; TITLE OF INVENTION: A METHOD FOR CLONING ACTIVE PROMOTERS  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/389,564B  
; FILING DATE: 16-FEB-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/932,485  
; FILING DATE: 19-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/496,155  
; FILING DATE: 19-MAR-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/044,077  
; FILING DATE: 29-APR-1987  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 86 10600  
; FILING DATE: 30-APR-1986  
; ATTORNEY/AGENT INFORMATION:  
; NAME: REED, GRANT E.  
; REGISTRATION NUMBER: 41,264

REFERENCE/DOCKET NUMBER: 1716.008000G  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1588 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-389-5648-16

Query Match 7.38; Score 34; DB 2; Length 1588;  
Best Local Similarity 44.18; Pred. No. 1.5; Mismatches 180; Indels 0; Gaps 0;  
Matches 142; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

QY 82 aacaaagccaaagttcatatcttcaagatcgccgatacaagaagaaggtgtcatcgac 141  
DB 643 AACGGACACCTCAACACTAGCCACAGGCTTCTGCTGCAACGAGATGATATCTGGAG 702  
QY 142 gaggtctcgcaagaagaaggaaggtctccgtacgaaggtcgaaggtaccgaagat 201  
DB 703 GCGAAGTCGAGGGGAGATGCTTGACCCCTCCTGCTGACGCGGCGGCTGGACTCT 762  
QY 202 agcaagaggtatcccgctctcgtatgacgtacagatgtcgaagtcagatcgtgtgac 261  
DB 763 GCCGGTTGCGGCTTCAACCCCTATGCGAGCGGCTACAAAGCTCTACGCGGCGGAGAT 822  
QY 262 ggtgaggaagaagaagaagatgtttcatctcctcgtggttcctcctaagacacactact 321  
DB 823 ACCGTTACACCTTCAACAGACCTTACCATCTACCCAGTTCAACAGGAGACGCGCTCG 882  
QY 322 ctgtgtcctatgatctacgcacacacagcagcaggaagacttgaagaagctctcaacacac 381  
DB 883 CCTCGGGCAACCTTGAGAGCATCACCCGCAAGTACAGCAAAAGGGGTGAGATCCCC 942  
QY 382 acctcatccagctgacgaca 403  
DB 943 AGCGCCAGCCCGGCGGCGACA 964

RESULT 21  
US-08-466-047B-16  
Sequence 16, Application US/08466047B  
GENERAL INFORMATION:  
APPLICANT: Nakari, Milja H.  
APPLICANT: Onnela, Milja-Leena  
APPLICANT: Ilm n, Marja H.  
APPLICANT: Nevalainen, Kaisa Milja Helena  
APPLICANT: Penttil, Merja E.  
TITLE OF INVENTION: Fungal Promoters Active In The Presence  
OF GLUCOSE  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
APPLICATION NUMBER: US/08/466,047B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/389,564

FILING DATE: 16-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/932,564  
FILING DATE: 19-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/496,155  
FILING DATE: 19-MAR-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/044,077  
FILING DATE: 29-APR-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 86 10600  
FILING DATE: 30-APR-1986  
ATTORNEY/AGENT INFORMATION:  
NAME: REED, GRANT E.  
REGISTRATION NUMBER: 41,264  
REFERENCE/DOCKET NUMBER: 1716.008000H  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1588 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-466-047B-16

Query Match 7.38; Score 34; DB 3; Length 1588;  
Best Local Similarity 44.18; Pred. No. 1.5; Mismatches 180; Indels 0; Gaps 0;  
Matches 142; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

QY 82 aacaaagccaaagttcatatcttcaagatcgccgatacaagaagaaggtgtcatcgac 141  
DB 643 AACGGACACCTCAACACTAGCCACAGGCTTCTGCTGCAACGAGATGATATCTGGAG 702  
QY 142 gaggtctcgcaagaagaaggaaggtctccgtacgaaggtcgaaggtaccgaagat 201  
DB 703 GCGAAGTCGAGGGGAGATGCTTGACCCCTCCTGCTGACGCGGCGGCTGGACTCT 762  
QY 202 agcaagaggtatcccgctctcgtatgacgtacagatgtcgaagtcagatcgtgtgac 261  
DB 763 GCCGGTTGCGGCTTCAACCCCTATGCGAGCGGCTACAAAGCTCTACGCGGCGGAGAT 822  
QY 262 ggtgaggaagaagaagaagatgtttcatctcctcgtggttcctcctaagacacactact 321  
DB 823 ACCGTTACACCTTCAACAGACCTTACCATCTACCCAGTTCAACAGGAGACGCGCTCG 882  
QY 322 ctgtgtcctatgatctacgcacacacagcagcaggaagacttgaagaagctctcaacacac 381  
DB 883 CCTCGGGCAACCTTGAGAGCATCACCCGCAAGTACAGCAAAAGGGGTGAGATCCCC 942  
QY 382 acctcatccagctgacgaca 403  
DB 943 AGCGCCAGCCCGGCGGCGACA 964

RESULT 22  
US-08-658-665-53  
Sequence 53, Application US/08658665  
Patent No. 5997878  
GENERAL INFORMATION:  
APPLICANT: Paolelli, Enzo  
APPLICANT: Pincus, Steven E.  
APPLICANT: Cox, William I.  
APPLICANT: Kaufman, Elizabeth K.  
TITLE OF INVENTION: Recombinant Poxvirus - Cytomegalovirus,  
AND ITS USES  
NUMBER OF SEQUENCES: 190  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Curtis, Morris & Safford, P.C.  
STREET: 530 Fifth Avenue

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Pred. No. 1.6;	Mismatches	72;	Indels	0;
Gaps	0;			
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Db	84	CGTGACCAAGCCACGACGTTCTCTGAGACTATGTTGAGAGAGATTAAGTACGTACGT	143	
QY	129	gattgtcatcgacagagcttcgcgaagaagaagatacagagctctccgtagcaggtccga	188	
Db	144	GAGTGTGGAGAACCCGCTGTTTCCAGAGTGTGGCCGACAGATCCCTCAAAACTTTTGAA	203	
QY	189	ggtaccgaagatagacagaggttaattcccg	217	

[illegible]

RESULT 24  
US-09-085-273-53  
Sequence 53, Application US/09085273  
Patent No. 6267965  
GENERAL INFORMATION:  
APPLICANT: Paoletti, Enzo  
APPLICANT: Pincus, Steven E.  
APPLICANT: Cox, William I.  
APPLICANT: Kaufman, Elizabeth K.  
TITLE OF INVENTION: RECOMBINANT POXYVIRUS - CYTOMEGALOVIRUS  
TITLE OF INVENTION: COMPOSITIONS AND USES  
NUMBER OF SEQUENCES: 176  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtiss, Morris & Safford  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/085,273  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,014  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Frommer Esq., William S.  
REGISTRATION NUMBER: 25,506  
REFERENCE/DOCKET NUMBER: 454310-2720







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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: January 29, 2002, 16:17:56 ; Search time 166.01 Seconds  
(without alignments)  
2401.399 Million cell updates/sec

Title: US-09-722-838-1

Perfect score: 465  
Sequence: 1 atggcgctgcgcgcgcgcgtgt.....gtggttaagccgcgtaataag 465

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues  
Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing First 45 summaries

Database : N.Geneseq.1101:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	282	60.6	801	21	AAFI2586
2	82	17.6	959	21	AAFO8519
3	39.4	8.5	4985	20	AAAX00463
4	38.6	8.3	458	21	AAAC39747
5	38.6	8.3	507	21	AAAC48124
6	36.6	7.9	3900	21	AAAC68343
7	36.4	7.8	489	21	AAAC35770
8	36.4	7.8	897	19	AAAV37146
9	36.2	7.8	897	22	AAH01741
10	36.2	7.8	1545	12	AAO14156
11	36.2	7.8	1683	15	AAO78255

12	36.2	7.8	1726	15	AAO78267	DNA encoding recom
13	36.2	7.8	1728	15	AAO78268	DNA encoding recom
14	36.2	7.8	1729	15	AAO78265	DNA encoding recom
15	36.2	7.8	1731	15	AAO78270	DNA encoding recom
16	36.2	7.8	1732	15	AAO78266	DNA encoding recom
17	36.2	7.8	1741	15	AAO78269	DNA encoding recom
18	36	7.7	2550	22	AAI61247	Human polynucleoti
19	36	7.7	3327	22	AAI59461	Human polynucleoti
20	35.2	7.6	789	21	AAFI4925	Trichoderma reesei
21	35.2	7.6	1709	20	AAAB0780	Cytokeratin 15 CDN
22	35.2	7.6	1709	20	AAAB32496	Seq ID No:11 used
23	35.2	7.6	1709	21	AAAI0426	Human cytochrome
24	35.2	7.6	2822	22	AAH21845	Rhodococcus sp. sm
25	34.6	7.4	2057	18	AAI45098	Cytomegalovirus po
26	34.4	7.4	2363	17	AAI58313	Oyster pearl prote
27	34.2	7.4	897	21	AAAC37858	Arabidopsis thalia
28	34	7.3	772	21	AAAC46548	zee may's DNA fragm
29	34	7.3	1292	21	AAAS8014	1292 bp candida al
30	34	7.3	1485	21	AAAC43775	zee may's DNA fragm
31	34	7.3	1588	15	AAO58010	Sequence of cellu
32	34	7.3	1588	21	AAAG95410	Trichoderma reesei
33	34	7.3	2942	21	AAZ48661	L. mycophilus chit
34	33.8	7.3	1032	21	AAFO7546	Fusarium venenatum
35	33.8	7.3	1386	18	AAI47543	Cytomegalovirus AD
36	33.8	7.3	1476	18	AAI47540	Human cytochrome
37	33.8	7.3	1740	19	AAV42803	Human CMV IE2 gene
38	33.8	7.3	1975	18	AAI47541	H6 promoted cyto
39	33.8	7.3	3351	20	AAZ31552	S. rochei strain E
40	33.8	7.3	3409	18	AAI47542	CMV IE1. Jacking a
41	33.8	7.3	3499	18	AAI47542	H6 promoted cyto
42	33.4	7.2	1155	21	AAFO7503	Fusarium venenatum
43	33.4	7.2	3258	22	AAH42269	Nucleotide sequenc
44	33.2	7.1	1942	17	AAI38896	Carnation ACC synt
45	33	7.1	1162	21	AAH9451	Rice branched chl

## ALIGNMENTS

RESULT 1	
AAFI2586	
ID AAFI2586 standard; cDNA; 801 BP.	
XX	
AC AAFI2586;	
XX	
DT 13-MAR-2001 (first entry)	
XX	
DE Aspergillus oryzae EST seq ID NO:5109.	
XX	
KW Multiple gene expression; filamentous fungal cell; EST;	
KW expressed sequence tag; Fusarium venenatum; Aspergillus niger;	
KW Aspergillus oryzae; Trichoderma reesei; Identification; recom	
KW culture condition; environmental stress; spore morphogenesis;	
KW metabolic pathway engineering; catabolic pathway engineering; ss.	
XX	
OS Aspergillus oryzae.	
XX	
PN WO200056762-A2.	
XX	
PD 28-SEP-2000.	
XX	
PF 22-MAR-2000; 2000MO-US07781.	
XX	
PR 22-MAR-1999; 99US-0273623.	
XX	
PA (NOVO ) NOVO NORDISK BIOTECH INC.	
PA (NOVO ) NOVO NORDISK AS.	
XX	
PI Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;	
XX	
DR WPI; 2000-594572/56.	
XX	
PT Monitoring differential expression of genes in filamentous fungal cells	



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Db      231  gaagcttaacagaagatcaacattcatctctacaaactctctgacgactacaaggagat 290
Qy      132  tgcatacgaagaggtctgcgcagaagaaggaactacgaaggtctctcgttcgacggtcgaagc 191
Db      291  tgttcgtcagaagaaggtctgcgcagaagaaggaactacgaaggtctctcgttcgacggtcgaagc 350
Qy      192  taccagaagatagaaggtgatccgc-----tctcgttatgtgagctaca 239
Db      351  cgtaccgccaagaagcgaactgtgtcgttcgcaagggtcccgcttaccgcttacaaga 410
Qy      240  tgcatacgaaggtctgcgcagaagaagaagaagaactgtttcactctctg 299
Db      411  ctccgagtaacaactcgtcctcgttcgcatgtatccgaaacaagatcacactcattgctctg 470
Qy      300  ggttcctcagacacactactctgtgtccatgatcttaagcagcaacgaggaact 359
Db      471  gtccctcgtatgtctgtgcacccaagatgatctacgcttccctcccaaggagacct 530
Qy      360  gaagaagacgtctca---acatccacacctccatccacgcttcgacgaagaagcgacattga 416
Db      531  taagcgtatcgtccacgcgcacatgcaccgaggtgcaggaaccaatgacactgatacaca 590
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Db      591  atacgacttcactcctcaagaaccgtcagcaagggt 624

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## RESULT 3

AAK00463  
AAK00463 standard; cDNA; 4985 BP.

AAK00463:

21-MAY-1999 (first entry)

Human type IX adenylyl cyclase cDNA.

Adenylyl cyclase type IX; human; hAC9; diagnosis; therapy; ss.

Homo sapiens.

Key CDS Location/Qualifiers

FT CDS 17..3901

FT CDS /'tag- a

MO9901540-A2.

14-JAN-1999.

01-JUL-1998; 98MO-US13541.

01-JUL-1997; 97US-0886440.

(CORP-) COR THERAPEUTICS INC.

(UNIT) UNIT WASHINGTON.

Hacker B, Strom DR, Tomlinson JA;

WPI; 1999-106043/09.

P-PSDB; AAW30601.

Newly isolated and purified human type IX adenylyl cyclase (hAC9)

polypeptide - useful for identifying potential therapeutic agents

hAC9-associated diseases and disorders

Claim 3; Fig 2A-I; 49pp; English.

from them in being larger, particularly in the C1b and C2b regions.  
hAC9 cDNA was initially isolated from a human heart cDNA library  
using an adenylyl cyclase type I PCR fragment as probe. Primers  
based on an isolated clone were used to obtain an overlapping clone  
and hence the full-length cDNA sequence. The invention relates to  
the hAC9 gene, methods for the recombinant production of purified  
hAC9 and the proteins made by these methods, antibodies against  
hAC9, vectors, probes and host cells (especially HEK-293) transformed  
by genes encoding polypeptides having hAC9 activity, along with  
diagnostic and therapeutic uses for these various reagents. hAC9  
can be used as a tool to screen for agonists and antagonists that  
stimulate/inhibit hAC9. Such compounds have therapeutic utility  
in treating diseases caused by aberrant activity of this enzyme,  
and diseases whose symptoms can be ameliorated by stimulating or  
inhibiting the activity of hAC9.

Sequence 4985 BP; 1097 A; 1472 C; 1378 G; 1038 T; 0 other;

Query Match 8.5%; Score 39.4; DB 20; Length 4985;  
Best Local Similarity 57.9%; Pred. NO. 0.13; Mismatches 0; Gaps 0;  
Matches 70; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

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Qy      328  tccatgatctacgcgcacacacgaggaacttgaagaagctctcaacatccacactcc 387
Db      3167  tccagaagaccacgacagcgaggggtgatctctgcgcacgcatcgaactcagcaggttc 3226
Qy      388  atccagcgtcagcagaagggcgacattgagtgaagaactgtctgcgcagagcgaggt 447
Db      3227  tacgagagaaactacgagggcgacagagagtgctacccggtcccaacagatcctcgg 3286
Qy      448  g 448
Db      3287  g 3287

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## RESULT 4

AAC39747  
AAC39747 standard; DNA; 458 BP.

AAC39747:

17-OCT-2000 (first entry)

Zea mays DNA fragment SEQ ID NO: 25751.

Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway; metabolic;

KW pathway; promoter; termination sequence; corn; ss.

Zea mays subsp. mays.

EP1033405-A2.

06-SEP-2000.

25-FEB-2000; 2000EP-0301439.

25-FEB-1999; 99US-0121825.

05-MAR-1999; 99US-0123180.

09-MAR-1999; 99US-0123548.

23-MAR-1999; 99US-0125788.

25-MAR-1999; 99US-0126284.

29-MAR-1999; 99US-0126785.

01-APR-1999; 99US-0127462.

06-APR-1999; 99US-0128234.

08-APR-1999; 99US-0128714.

16-APR-1999; 99US-0129845.

19-APR-1999; 99US-0130077.

21-APR-1999; 99US-0130449.

23-APR-1999; 99US-0130510.

23-APR-1999; 99US-0130891.

28-APR-1999; 99US-0131449.

PR 30-APR-1999; 99US-0132048.  
PR 30-APR-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
PR 05-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 07-MAY-1999; 99US-0132487.  
PR 11-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 18-JUN-1999; 99US-0139817.  
PR 21-JUN-1999; 99US-0139889.  
PR 22-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140685.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0143542.  
PR 13-JUL-1999; 99US-0143624.  
PR 14-JUL-1999; 99US-0144005.  
PR 15-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0144814.  
  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145224.  
PR 23-JUL-1999; 99US-0145226.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148341.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149475.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151067.  
PR 30-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153758.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154019.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.  
PR 23-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0159283.  
PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159329.  
PR 14-OCT-1999; 99US-0159330.  
PR 14-OCT-1999; 99US-0159331.  
PR 14-OCT-1999; 99US-0159637.  
PR 14-OCT-1999; 99US-0159638.  
PR 18-OCT-1999; 99US-0159584.

PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160767.  
PR 21-OCT-1999; 99US-0160768.  
PR 21-OCT-1999; 99US-0160770.  
PR 21-OCT-1999; 99US-0160814.  
PR 21-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160980.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.  
PR 25-OCT-1999; 99US-0161404.  
PR 25-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 8.3%; Score 38.6; DB 21; Length 458;  
Best Local Similarity 52.3%; Pred. No. 0.085;  
Matches 148; Conservative 0; Mismatches 114; Indels 21; Gaps 2;

QY 93 gtccatatttcgaagtcgcgataacaagaagtggtctgctacgaggtctcgca 152  
DB 123 gtatgtatcttcacagtcacgacagtagagaggtctgctgcacagatcgcg 182  
QY 153 agaaagagctacagcttcctcgtagcagctcgagctacaggaataaggttaa 212  
DB 183 gcccgaggagagctacagacacttcaacgctcgctaccacgactatgctg 234  
QY 213 tcccgctctctgtatgacgtacgaatgctcgaatcgtggtcggtgagga 272  
DB 235 -----cgtaacgctctacgactcgtatgctg-----taagcagcaactg 281  
QY 273 gagaagaagattgttctctctctgttccctcctcagacactactctgtgtcat 332  
DB 282 gaaagaagaatttctctctctctctctctctcctcctcgtacgtcgtcgaagac 341  
QY 333 gatctacgcacagcagcgaggaactggaagacgctctcaac 375  
DB 342 catatatccgtgtcaaggaaccaattcgtcatgagcttgac 384

## RESULT 5

AAC48124

AAC48124 standard; DNA; 507 BP.

AAC48124;

18-OCT-2000 (first entry)

Zea mays DNA fragment SEQ ID NO: 56350.

Hybridisation assay; genetic mapping; gene expression control;

Protein Identification; signal transduction pathway; metabolic;

pathway; promoter; termination sequence; corn; ss.

Zea mays subsp. mays.

EPI033405-A2.

25-FEB-2000; 2000EP-0301439.

25-FEB-1999; 99US-0121925.

05-MAR-1999; 99US-0123180.

09-MAR-1999; 99US-0123548.

23-MAR-1999; 99US-0125788.

25-MAR-1999; 99US-0126264.

PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 23-APR-1999; 99US-0130891.  
PR 28-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 30-APR-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
PR 05-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 06-MAY-1999; 99US-0132487.  
PR 07-MAY-1999; 99US-0132863.  
PR 11-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135253.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137502.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139819.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140655.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.



PF 19-APR-2000; 2000MO-US10644.  
XX 22-APR-1999; 99US-0296906.  
PR 22-JUN-1999; 99US-0337976.  
XX (ZYMO) ZYMOGENETICS INC.  
XX  
PI Lok S, Whitmore TE;  
DR WPI; 2000-687365/67.  
XX  
PT Detecting a chromosome 1q21-q24 abnormality for diagnosing metabolic  
PT disease, such as human obesity and diabetic disorders, comprises  
PT examining insulin receptor-related receptor gene and its gene products  
XX  
XX Disclosure; Page 86-87; 11pp; English.  
XX  
XX The present invention relates to insulin receptor-related receptor  
CC (IRRR). Mutations in this gene indicate a chromosome 1q21-q24  
CC abnormality. IRRR polypeptides and DNA may be useful in the diagnosis of  
CC disorders associated with abnormal expression of the IRRR protein,  
CC for example obesity, dyslipidemia and diabetes.  
XX  
SQ Sequence 3900 BP; 593 A; 421 C; 728 G; 517 T; 1641 other;  
  
Query Match 7.9%; Score 36.6; DB 21; Length 3900;  
Best Local Similarity 29.0%; Pred. No. 0.78;  
Matches 60; Conservative 37; Mismatches 110; Indels 0; Gaps 0;  
  
QY 41 ttactgcatcaagattccgctgagcgagcaacaaagcgcaacaagcaagtcattca 100  
DB 2189 tnaenwnatnaaayaaayaaayccncaingaywngarmngaymgngngaracngny 2248  
QY 101 tctcaagatcgccgatacaagaagaggtgtgcatcgacgagctctcgcaagaagag 160  
DB 2249 tnytmngnytcngnaaaraayaaywngaytytgatrchaygarayaaarctnccmng 2308  
QY 161 actagaggtctctcgtagcagctcgagctaccagaagatagcaaggtatcccgctc 220  
DB 2309 armngngcngtntwngngnytmngcaytlyacngartaymgatthgaythcaygnt 2368  
QY 221 ctggtatcgactacagatgcaggt 247  
DB 2369 gyaaycaycngcncaycngtngnt 2395  
  
RESULT 7  
AAC35770  
ID AAC35770 standard; DNA; 489 BP.  
XX  
AC AAC35770;  
XX  
DT 17-OCT-2000 (first entry)  
XX  
DE Zea mays DNA fragment SEQ ID NO: 11360.  
XX  
XX Hybridisation assay; genetic mapping; gene expression control;  
KM protein identification; signal transduction pathway; metabolic;  
KM pathway; promoter; termination sequence; corn; ss.  
XX  
OS Zea mays subsp. mays.  
XX  
PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-0301439.  
XX  
XX 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126254.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 28-APR-1999; 99US-0130891.  
PR 30-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 30-APR-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
PR 05-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 06-MAY-1999; 99US-0132487.  
PR 07-MAY-1999; 99US-0132863.  
PR 11-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139452.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139889.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.





XX PI Bergeron MG, Ouellette M, Picard FJ, Roy PH.  
 XX DR WPI: 1998-286967/25.  
 XX PT Use of oligo:nucleotide primers and probes - for detection,  
 XX PT identification and quantification of bacteria, fungi and bacterial  
 XX PT antibiotic resistance gene(s)  
 XX PS Claim 12: Pages 134-135; 167pp; English.  
 XX CC The present sequence was used to design primers and probes used in the  
 XX CC course of the invention. The specification describes the use of probes  
 XX CC and/or amplification primers which are specific, ubiquitous and sensitive  
 XX CC for determining the presence and amount of nucleic acids from a bacterial  
 XX CC antibiotic resistance gene and specific bacterial and fungal species in  
 XX CC any sample suspected of containing the bacterial or fungal nucleic acids,  
 XX CC where each of the nucleic acid or variant or part comprises a selected  
 XX CC target region hybridisable with the probes or primers. The method of  
 XX CC use comprises contacting the sample with the probes or primers and  
 XX CC detecting the presence of hybridised probes or amplified products as an  
 XX CC indication of the presence of the specific bacterial or fungal species  
 XX CC and bacterial antibiotic resistance genes. The methods and products can  
 XX CC be used to detect and identify the bacterial and fungal species and  
 XX CC genera and determine the bacterial resistance to antibiotics.  
 XX SQ Sequence 897 BP; 173 A; 265 C; 271 G; 188 T; 0 other;

Query Match 7.8%; Score 36.4; DB 19; Length 897;  
 Best Local Similarity 58.2%; Pred. No. 0.5;  
 Matches 64; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 91 aagtcattatcttcgaagtcgcgatacaagaagaaggtgttcacgaggtctcg 150  
 ||||| | ||||| ||||| | ||||| | ||||| |||||  
 Db 201 AAGTTCGGCACTTCAGCTCGACGAGCTCGAAGAGCTCGGCTGCACTGCTGCAC 142  
 ||||| | ||||| ||||| | ||||| | ||||| |||||  
 QY 151 caagaagaagagtagcaggtcttcgtagcaggtcgcaggtacccaaga 200  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 141 CTGTGTGAGAACACGACGATGGCCGGAACGCCACCTGACGGGCAACCA 92  
 ||||| | | | | | | | | | | | | | | | | | |

RESULT 9  
 AAH01741/C  
 ID AAH01741 standard; DNA: 897 BP.  
 XX AC AAH01741;  
 XX DT 24-JUL-2001 (first entry)  
 XX DE Agrobacterium tumefaciens nucleotide sequence SEQ ID NO:1734.  
 XX KM Species specific; genus specific; family specific; probe: detection;  
 XX KM Identification: algal; archaeal; bacterial; fungal; parasitica;  
 XX KM microorganism; diagnosis; translation elongation factor Tu; toxin;  
 XX KM translation elongation factor G; RecA recombinase; resistance;  
 XX KM catalytic subunit of proton-translocating ATPase; antimicrobial;  
 XX KM vaccine; primer; ds.  
 XX OS Agrobacterium tumefaciens.  
 XX PN WO200123604-A2.  
 XX PD 05-APR-2001.  
 XX PF 28-SEP-2000; 2000WO-CA01150.  
 XX PR 28-SEP-1999; 99CA-2283458.  
 XX PR 19-MAY-2000; 2000CA-2307010.  
 XX PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.  
 XX PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;

PI Picard FJ, Roy PH;  
 XX DR WPI: 2001-245006/25.  
 XX PT Nucleic acid sequences are used to generate universal probes and  
 XX PT primers which can be used to identify and detect the presence of algal,  
 XX PT archaeal, bacterial, fungal and parasitica species in a test sample -  
 XX PS Disclosure; Page 1307; 1580pp; English.  
 XX CC The present invention describes a method for generating a repository of  
 XX CC nucleic acids of tuf, fus, alpd and/or recA genes from which probes  
 XX CC and/or primers are derived. The method comprises amplifying the nucleic  
 XX CC acids of determined algal, archaeal, bacterial, fungal and parasitica  
 XX CC species with a combination of defined primer pairs. The method can be  
 XX CC used for producing probes and/or primers for detecting one or more  
 XX CC related microorganisms e.g. algae, archaea, bacteria, fungi and  
 XX CC parasites, for universal detection and for specific and ubiquitous  
 XX CC detection and identification of an algal, archaeal, bacterial, fungal  
 XX CC and parasitica species, genus, family and group. A nucleic acid (I)  
 XX CC obtained using the method of the invention can be used for the universal  
 XX CC detection of any bacterium, fungus or parasite in a sample and for the  
 XX CC detection of at least one antimicrobial agent resistance gene or at  
 XX CC least one toxin gene. hexa nucleic acids are used for the specific and  
 XX CC ubiquitous detection and for identification of Streptococcus pneumoniae.  
 XX CC (I) can be used to design a therapeutic agent which is effective against  
 XX CC microorganisms. Microbial species or genus or family or phylum or group  
 XX CC which can be detected include Abiotrophia adiacens, Bordetella sp.,  
 XX CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,  
 XX CC Mycobacteriaceae family, Pseudomonas group, Streptococcus sp.,  
 XX CC Neisseria gonorrhoeae and Staphylococcus sp.. Using DNA based tests  
 XX CC provides faster results than substrate specificity tests as results can  
 XX CC be determined in an hour and improved accuracy is also achieved.  
 XX CC AAH00010 to AAH002304 represent nucleotide sequences and primers/probes  
 XX CC which are given in the exemplification of the present invention.  
 XX SQ Sequence 897 BP; 173 A; 265 C; 271 G; 188 T; 0 other;

Query Match 7.8%; Score 36.4; DB 22; Length 897;  
 Best Local Similarity 58.2%; Pred. No. 0.5;  
 Matches 64; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 91 aagtcattatcttcgaagtcgcgatacaagaagaaggtgttcacgaggtctcg 150  
 ||||| | ||||| ||||| | ||||| | ||||| |||||  
 Db 201 AAGTTCGGCACTTCAGCTCGACGAGCTCGAAGAGCTCGGCTGCACTGCTGCAC 142  
 ||||| | ||||| ||||| | ||||| | ||||| |||||  
 QY 151 caagaagaagagtagcaggtcttcgtagcaggtcgcaggtacccaaga 200  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 141 CTGTGTGAGAACACGACGATGGCCGGAACGCCACCTGACGGGCAACCA 92  
 ||||| | | | | | | | | | | | | | | | | | |

RESULT 10  
 AAQ14156  
 ID AAQ14156 standard; DNA: 1545 BP.  
 XX AC AAQ14156;  
 XX DT 03-JAN-1992 (first entry)  
 XX DE Clone pNH10 encoding cholesterol oxidase II.  
 XX KM CMO; ss.  
 XX OS Brevibacterium sterolicum ATCC 21387.  
 XX PN EP452112-A.  
 XX FT Key 1..1545 Location/Qualifiers  
 XX FT CDS /\*tag= a  
 XX PD 16-OCT-1991.



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XX PN W09425603-A.
XX PD 10-NOV-1994.
XX PF 02-MAY-1994; 94WO-EP01394.
XX PR 05-MAY-1993; 93DE-4314793.
XX PR 09-DEC-1993; 93DE-4342012.
XX PA (BOEF ) BOEHRINGER MANNHEIM GMBH.
XX PI Jarsch M;
XX DR WPI; 1994-358279/44.
XX DR P-PSDB; AAR65958.
XX PT New cholesterol oxidase from Brevibacterium sterolicum - and
XX PT related DNA and recombinant enzyme, useful for cholesterol assay,
XX PT has high cholesterol affinity and can be produced in large amts.
XX PT as cytoplasmic enzyme.
XX PS Claim 6; Page 39-41; 83pp; German.
XX CC AAQ78265-70 encode recombinant cholesterol oxidases, and contain a
XX CC supplementary in-frame 5' sequence which contains a translation start
XX CC codon. The peptide that this encodes replaces the normal signal
XX CC sequence (sic). Recombinant cholesterol oxidases are useful in
XX CC cholesterol assays, as the enzyme has high cholesterol affinity and
XX CC can be produced in large amts. as a cytoplasmic enzyme.
XX SQ Sequence 1726 BP; 327 A; 601 C; 537 G; 261 T; 0 other;

Query Match          7.8%; Score 36.2; DB 15; Length 1726;
Best Local Similarity 53.1%; Pred. No. 0.74; Mismatches 68; Indels 0; Gaps 0;
Matches 77; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 51 caacgattccgcatgagcggaacaaggccaagaagcgaatcattatcttcaagat 110
   ||| ||||| ||||| ||| ||| ||| ||| |||
Db 220 ctacaagatccgcgcgcgcgcgcatgcaagctgagcccgctcacacgtyggaaggg 279

QY 111 gcccgataacaagaagaggtgttcattcgaagaggtctcgcaagaagaggaactaagagt 170
   ||| ||| ||||| ||| ||| ||| ||| ||| |||
Db 280 ggcacaagtcgagaaggtgtatcctcgccgacacgatacgatctgaacgagcaccagct 339

QY 171 ctccgtagcagagctcgaggtacc 195
   || ||| ||||| |||
Db 340 gaacacggcgcccgctggtacc 364

RESULT 13
AAQ78268
ID AAQ78268 standard; DNA: 1728 BP.
AC AAQ78268;
XX
XX 04-AUG-1995 (first entry)
XX
XX DNA encoding recombinant cholesterol oxidase.
XX
XX cholesterol oxidase; enzymatic test; assay; cholesterol determination;
XX high affinity; cytoplasmic enzyme; signal peptide; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX CDS 19..1728
XX FT /*tag= a
XX FT /note= "Immature cholesterol oxidase"
XX FT misc_difference 19..45
XX FT /*tag= b
XX FT /note= "supplementary, in-frame 5' sequence
```

```
FT FT sig_peptide 46..201 contg. a translation start codon"
FT FT /*tag= c
FT FT mat_peptide 202..1728
FT FT /*tag= d
FT FT /note= "mature cholesterol oxidase"
XX
XX W09425603-A.
XX PD 10-NOV-1994.
XX PF 02-MAY-1994; 94WO-EP01394.
XX PR 05-MAY-1993; 93DE-4314793.
XX PR 09-DEC-1993; 93DE-4342012.
XX PA (BOEF ) BOEHRINGER MANNHEIM GMBH.
XX PI Jarsch M;
XX DR WPI; 1994-358279/44.
XX DR P-PSDB; AAR65959.
XX PT New cholesterol oxidase from Brevibacterium sterolicum - and
XX PT related DNA and recombinant enzyme, useful for cholesterol assay,
XX PT has high cholesterol affinity and can be produced in large amts.
XX PT as cytoplasmic enzyme.
XX PS Claim 6; Page 44-46; 83pp; German.
XX CC AAQ78265-70 encode recombinant cholesterol oxidases, and contain a
XX CC supplementary in-frame 5' sequence which contains a translation start
XX CC codon. The peptide that this encodes replaces the normal signal
XX CC sequence (sic). Recombinant cholesterol oxidases are useful in
XX CC cholesterol assays, as the enzyme has high cholesterol affinity and
XX CC can be produced in large amts. as a cytoplasmic enzyme.
XX SQ Sequence 1728 BP; 327 A; 601 C; 537 G; 263 T; 0 other;

Query Match          7.8%; Score 36.2; DB 15; Length 1728;
Best Local Similarity 53.1%; Pred. No. 0.74; Mismatches 68; Indels 0; Gaps 0;
Matches 77; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 51 caacgattccgcatgagcggaacaaggccaagaagcgaatcattatcttcaagat 110
   ||| ||||| ||||| ||| ||| ||| ||| |||
Db 222 ctacaagatccgcgcgcgcgcgcatgcaagctgagcccgctcacacgtyggaaggg 281

QY 111 gcccgataacaagaagaggtgttcattcgaagaggtctcgcaagaagaggaactaagagt 170
   ||| ||| ||||| ||| ||| ||| ||| ||| |||
Db 282 ggcacaagtcgagaaggtgtatcctcgccgacacgatacgatctgaacgagcaccagct 341

QY 171 ctccgtagcagagctcgaggtacc 195
   || ||| ||||| |||
Db 342 gaacacggcgcccgctggtacc 366

RESULT 14
AAQ78265
ID AAQ78265 standard; DNA: 1729 BP.
AC AAQ78265;
XX
XX 03-AUG-1995 (first entry)
XX
XX DNA encoding recombinant cholesterol oxidase.
XX
XX cholesterol oxidase; enzymatic test; assay; cholesterol determination;
XX high affinity; cytoplasmic enzyme; signal peptide; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX CDS 19..1728
XX FT /*tag= a
XX FT /note= "Immature cholesterol oxidase"
XX FT misc_difference 19..45
XX FT /*tag= b
XX FT /note= "supplementary, in-frame 5' sequence
```

[illegible]

KW	cholesterol oxidase; enzymatic test; assay; cholesterol determination;
KM	high affinity; cytoplasmic enzyme; signal peptide; ss.
XX	
OS	Synthetic.
XX	
FH	Location/Qualifiers
FT	25..1731
FT	CD5
FT	/*tag= "a
FT	/note= "immature cholesterol oxidase"
FT	25..48
FT	/*tag=
FT	/note=
FT	b
FT	"supplementary, in-frame 5' sequence
FT	conty. a translation start codon"
FT	49..201
FT	/*tag= c
FT	202..1731
FT	/*tag= d
FT	/note= "mature cholesterol oxidase"
FT	

PN WO94255603-A.  
 PD 10-NOV-1994.  
 XX  
 XX  
 PF 02-MAY-1994; 94WO-EP01394.  
 XX  
 XX  
 PR 05-MAY-1993; 93DE-4314793.  
 PR 09-DEC-1993; 93DE-4342012.  
 XX  
 XX  
 PA (BOE ) BOEHRINGER MANNHEIM GMBH.  
 XX  
 PI Jarsch M;  
 PI  
 DR WPI; 1994-358279/44.  
 DR P-PADB; AAR65961.  
 XX  
 PT New cholesterol oxidase from Brevibacterium sterolicum - and  
 PT related DNA and recombinant enzyme, useful for cholesterol assay,  
 PT has high cholesterol affinity and can be produced in large amts.  
 PT as cytoplasmic enzyme.  
 XX  
 PS  
 PS Claim 6; Page 53-55; 83pp; German.  
 CC  
 CC AA078265-70 encode recombinant cholesterol oxidases, and contain a  
 CC supplementary in-frame 5' sequence which contains a translation start  
 CC codon. The peptide that this encodes replaces the normal signal  
 CC sequence (s1c). Recombinant cholesterol oxidases are useful in  
 CC cholesterol assays, as the enzyme has high cholesterol affinity and  
 CC can be produced in large amts. as a cytoplasmic enzyme.  
 CC  
 CC  
 CC Sequence 1731 BP; 328 A; 605 C; 536 G; 262 T; 0 other;  
 SQ

```

Query Match          7.88; Score 36.2; DB 15; Length 1731;
Best Local Similarity 53.1%; Pred. No. 0.74; Mismatches 68; Indels 0; Gaps 0;
Matches 77; Conservative 0;
QY      51 caacgatttcgcgatggcggccaacaggccacaacaaagttcatatcttcaaat 110
        ||| | | | | | | | | | | | | | | | | | | | | | | | | |
Db       225 ctacaagaatccgcccgccgcgcgcgaatgcacagcgttgaccgcccgctggaagaag 284
        ||| | | | | | | | | | | | | | | | | | | | | | | | | |
QY      111 cgcgcataacaagaagagagtgtgcatacgcagaggttcgcaagaagaagactacgaagt 170
        ||| | | | | | | | | | | | | | | | | | | | | | | | | |
Db       265 ggcacagctgcagaaggtgacctccgcgcgaacagatgacgacttgaaagcgatcacglt 344
        ||| | | | | | | | | | | | | | | | | | | | | | | | | |
QY      171 ctccgtagcagagctcgaaggtacc 195
        | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       345 gaacacggcgcgcccgtcgctaac 369
        | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 16
AAO78266
ID      AAO78266 standard; DNA; 1732 BP.
XX

```

AC	AA078266;
XX	
DT	04-AUG-1995 (first entry)
XX	
DE	DNA encoding recombinant cholesterol oxidase.
XX	
KW	cholesterol oxidase; enzymatic test; assay: cholesterol determination;
KW	high affinity; cytoplasmic enzyme; signal peptide; ss.
XX	
OS	Synthetic.
XX	
FH	Key
FT	CDS
FT	
FT	Location/Qualifiers
FT	20..1729
FT	/*tag= a
FT	/note= "Immature cholesterol oxidase"
FT	20..49
FT	/*tag= b
FT	/note= "supplementary, in-frame 5' sequence
FT	contg. a translation start codon"
FT	sig_peptide
FT	50..205
FT	/*tag= c
FT	mat_peptide
FT	206..1732
FT	/*tag= d
FT	/note= "mature cholesterol oxidase"
XX	
PN	W09425603-A.
XX	
PD	10-NOV-1994.
XX	
PE	02-MAY-1994; 94WO-EP01394.
XX	
PR	05-MAY-1993; 93DE-4314793.
PR	09-DEC-1993; 93DE-4342012.
XX	
PA	(BOEF ) BOEHRINGER MANNHEIM GMBH.
XX	
PI	Jarsch M;
XX	
DR	WPI; 1994-358279/44.
DR	P-PSDB; AAR65957.
XX	
PT	New cholesterol oxidase from <i>Brevibacterium sterolicum</i> - and
PT	related DNA and recombinant enzyme, useful for cholesterol assay,
PT	has high cholesterol affinity and can be produced in large amts.
PT	as cytoplasmic enzyme.
XX	
PS	Claim 6; Page 35-37; 83pp; German.
XX	
CC	AA078265-70 encode recombinant cholesterol oxidases, and contain a
CC	supplementary in-frame 5' sequence which contains a translation start
CC	codon. The peptide that this encodes replaces the normal signal
CC	sequence (sic). Recombinant cholesterol oxidases are useful in
CC	cholesterol assays, as the enzyme has high cholesterol affinity and
CC	can be produced in large amts. as a cytoplasmic enzyme.
XX	
XX	Sequence 1732 BP; 328 A; 604 C; 537 G; 263 T; 0 other;
XX	
SO	
Query Match 7.8%; Score 36.2; DB 15; Length 1732;	
Best Local Similarity 53.1%; Pred. No. 0.74; Mismatches 68; Indels 0; Gaps 0;	
Matches 77; Conservative 0;	
QY	51 caacagattccgcagatgcgcgaacaagccacaagaaccagattcatattccaagt 110
Db	226 tacaagaatccgcccgcgcgcgatgcacagcgtcggaaccgccctcacccgtgagaaggg 285
QY	111 cgcgcataacaagaaggaggttcatacgcagcagaggtctcgcaagaagacgactcagagt 170
Db	286 ggcacaagtcgcgaaggatcatctcgcgcgacacagattgacgacatctgaacgcgatacaggt 345
QY	171 ctccgctagcagagctcgcaggtcacc 195
Db	346 gaacacagggcgcgccctggtctacc 370

[illegible]

Db 295 ggcacagctcgagaagcgatccgcgcgaacagatgacgacatctgacgacgacggt 354  
 Oy 171 ctccgtacgagctcgaggtacc 195  
 Db 355 gaacacgagcgagcccgctggtacc 379

## RESULT 18

AAI61247

ID AAI61247 standard; cDNA: 2550 BP.

AAI61247;

22-OCT-2001 (first entry)

Human polynucleotide SEQ ID NO 5236.

Human; nootropic; immunosuppressant; cytoskeletal; gene therapy; cancer;  
 peripheral nervous system; neuropathy; central nervous system; CNS;  
 Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
 chemokine; thrombolytic; drug screening; arthritis; inflammation;  
 leukaemia; ss.

Homo sapiens.

WO200153312-A1.

26-JUL-2001.

26-DEC-2000; 2000WO-US34263.

21-JAN-2000; 2000US-0488725.  
 25-APR-2000; 2000US-0552317.  
 09-JUL-2000; 2000US-0598042.  
 19-JUL-2000; 2000US-0620312.  
 03-AUG-2000; 2000US-0653450.  
 14-SEP-2000; 2000US-0662191.  
 19-OCT-2000; 2000US-0693036.  
 29-NOV-2000; 2000US-0727344.

(HYSE-) HYSEQ INC.

Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;  
 Zhao QA, Zhou P, Goodrich R, Drmanac RT;

WPI: 2001-442253/47.

P-PSDB; AAM42091.

Novel nucleic acids and polypeptides, useful for treating disorders  
 such as central nervous system injuries -

Claim 1; SEQ ID NO 5236; 10078pp; English.

The invention relates to human nucleic acids (AAI57798-AAI61369) and  
 the encoded polypeptides (AAM38642-AAM42213) with nootropic,  
 immunosuppressant and cytoskeletal activity. The polynucleotides are useful  
 in gene therapy. A composition containing a polypeptide or polynucleotide  
 of the invention may be used to treat diseases of the peripheral nervous  
 system, such as peripheral nervous injuries, peripheral neuropathy and  
 localized neuropathies and central nervous system diseases, such as  
 Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 utilisation of the activities such as: immune system suppression,  
 activation/inhibition activity, chemotactic/chemokinetic activity, haemostatic  
 and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 assays for receptor activity, arthritis and inflammation, leukaemia and  
 C.N.S disorders.  
 Note: The sequence data for this patent did not form part of the printed  
 specification.

SQ Sequence 2550 BP; 633 A; 686 C; 650 G; 581 T; 0 other;

Query Match 7.7%; Score 36; DB 22; Length 2550;

Best Local Similarity 51.9%; Fred. No. 0.99; Mismatches 0; Gaps 0;

Matches 81; Conservative 0; Indels 75; Indels 0; Gaps 0;

Oy 65 tgagcgagcaacaaggccaagaacgaattatcttcaatgaatcgcgataacaaga 124  
 Db 663 tgcgcctccaagctgcgaacacatgctgctgggaagatctggaagctgacgacattgaca 722  
 Oy 125 aggaaggtgtcatcgacgagctctcgcaagaagagactagaggtctccgtacgaagc 184  
 Db 723 aggatgcatgctgcgacgacgaggttgcacgtgccaacacactcaaatcaagc 782  
 Oy 185 tcgaggtaccgaagatagcaaggggaatcccgctc 220  
 Db 783 tggaggggcagcagctgcccaacgagctgctcgccc 818

## RESULT 19

AAI59461

ID AAI59461 standard; cDNA: 3327 BP.

AAI59461;

22-OCT-2001 (first entry)

Human polynucleotide SEQ ID NO 1664.

Human; nootropic; immunosuppressant; cytoskeletal; gene therapy; cancer;  
 peripheral nervous system; neuropathy; central nervous system; CNS;  
 Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
 chemokine; thrombolytic; drug screening; arthritis; inflammation;  
 leukaemia; ss.

Homo sapiens.

WO200153312-A1.

26-JUL-2001.

26-DEC-2000; 2000WO-US34263.

21-JAN-2000; 2000US-0488725.  
 25-APR-2000; 2000US-0552317.  
 09-JUL-2000; 2000US-0598042.  
 19-JUL-2000; 2000US-0620312.  
 03-AUG-2000; 2000US-0653450.  
 14-SEP-2000; 2000US-0662191.  
 19-OCT-2000; 2000US-0693036.  
 29-NOV-2000; 2000US-0727344.

(HYSE-) HYSEQ INC.

Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;  
 Zhao QA, Zhou P, Goodrich R, Drmanac RT;

WPI: 2001-442253/47.

P-PSDB; AAM40305.

Novel nucleic acids and polypeptides, useful for treating disorders  
 such as central nervous system injuries -

Claim 1; SEQ ID NO 1664; 10078pp; English.

The invention relates to human nucleic acids (AAI57798-AAI61369) and  
 the encoded polypeptides (AAM38642-AAM42213) with nootropic,  
 immunosuppressant and cytoskeletal activity. The polynucleotides are useful  
 in gene therapy. A composition containing a polypeptide or polynucleotide  
 of the invention may be used to treat diseases of the peripheral nervous

CC system, such as peripheral nervous injuries, peripheral neuropathy and  
CC localised neuropathies and central nervous system diseases, such as  
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
CC utilisation of the activities such as: Immune system suppression,  
CC activating/inhibiting chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
CC assays for receptor activity, arthritis and inflammation, leukaemias and  
CC C.N.S disorders.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification.

CC Sequence 3327 BP; 814 A; 900 C; 880 G; 733 T; 0 other;

Query Match 7.7%; Score 36; DB 22; Length 3327;  
Best Local Similarity 51.9%; Pred. No. 1.1;  
Matches 81; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 65 tggagcgcaacaagcgcaacaagcacaagctcttcttcttcaagatcgccgataacaga 124  
DB 1431 tggcgcccaagctgcccacaagctgctgggcaagatctggaagctggccgacattgaca 1490  
QY 125 aggaaggtgtcatcgacgaagctctcgcaagaagagactacgagctcttcgtaagcagc 184  
DB 1491 aggatgcatgctgctggaagcagcagcttctgctgctgctgctgctgctgctgctgctg 1550  
QY 185 tggagctaccagaagatagcagaaggtatccgctc 220  
DB 1551 tggagggcgacagcgtgcccacagcagctgctgccc 1586

## RESULT 20

ID AAF14925 standard; cDNA; 799 BP.

AC AAF14925;

DT 13-MAR-2001 (first entry)

DE Trichoderma reesei EST SEQ ID NO:7448.

XX Multiple gene expression; filamentous fungal cell; EST;  
XX expressed sequence tag; Fusarium venenatum; Aspergillus niger;  
XX Aspergillus oryzae; Trichoderma reesei; identification; recombination;  
XX culture condition; environmental stress; spore morphogenesis;  
XX metabolic pathway engineering; catabolic pathway engineering; ss.

OS Trichoderma reesei.

PN WO200056762-A2.

PD 28-SEP-2000.

PF 22-MAR-2000; 2000WO-US07781.

PR 22-MAR-1999; 99US-0273623.

PA (NOVO ) NOVO NORDISK BIOTECH INC.

PA (NOVO ) NOVO NORDISK AS.

PI Berta RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;

DR WPI; 2000-594572/56.

PT Monitoring differential expression of genes in filamentous fungal cells  
PT uses fluorescence-labeled nucleic acids isolated from the cells and a  
PT substrate of expressed sequence tags -

PS Claim 89; Page 3008; 3161pp; English.

CC The present invention describes a method for monitoring differential  
CC expression of genes in a first filamentous fungal (FF) cell relative to

CC expression of the same genes in one or more second filamentous fungal  
CC cells. The method uses fluorescence-labeled nucleic acids isolated from  
CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs  
CC are used in the methods for monitoring differential expression of genes  
CC in a first filamentous fungal (FF) cell relative to expression of the  
CC same genes in one or more second filamentous fungal cells. Monitoring  
CC the global expression of genes from FF cells allows the production  
CC potential of the microorganisms to be improved. New genes may be  
CC discovered, possible functions of unknown open reading frames can be  
CC identified and gene copy number variation and stability can be  
CC monitored. The expression of genes can be used to study how FF cells  
CC adapt to changes in culture conditions, environmental stress, spore  
CC morphogenesis, recombination, metabolic or catabolic pathway  
CC engineering. Using ESTs provides several advantages over genomic or  
CC random cDNA clones including elimination of redundancy as one spot on an  
CC array equals one gene or open reading frame, and organisation of the  
CC microarrays based on function of the gene products to facilitate  
CC analysis of the results. AAF07478 to AAF11247 represents ESTs from  
CC Fusarium venenatum; AAF11248 to AAF1853 represents ESTs from Aspergillus  
CC niger; AAF1854 to AAF14878 represents ESTs from Aspergillus oryzae; and  
CC AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are  
CC all specifically claimed in the present invention.

CC Sequence 799 BP; 179 A; 246 C; 218 G; 150 T; 6 other;

Query Match 7.6%; Score 35.2; DB 21; Length 799;  
Best Local Similarity 45.8%; Pred. No. 1.1;  
Matches 121; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

QY 181 aggcctcgagctcaacagatagagaaggtatccgcgctcctctgtatgacatcagat 240  
DB 311 atgattcaaggcgccgacttaccagaaggcgatgagccggtgcaagctgacatccagc 370  
QY 241 gtcgagtcacatctcggtggtgaggaagaaagacagatgtttcatctctcg 300  
DB 371 aacaagtcagaagcagcacttcaagctgaaagcacaagaagggcgtctgcatg 430  
QY 301 gttccctcaacacactactctgtgtccatgatctacgaccagaacagggagaactg 360  
DB 431 gccaacgcyggaaccgacacacagcgtccagttcttcaaccactgtgttacctca 490  
QY 361 aagaagctctcaacatcacacactcattcacgcgtgacgaagaagggcgacattgag 420  
DB 491 tggctcgagggccgacacgctcgtcttcgaggggttctcgagggtcagacattgttgg 550  
QY 421 aagactgttctgcccgaagccagc 444  
DB 551 aagattgaaaagcttcagacgcgc 574

## RESULT 21

ID AAX80780 standard; cDNA; 1709 BP.

AC AAX80780;

DT 26-OCT-1999 (first entry)

DE Cytokeratin 15 cDNA.

XX Cytokeratin 15; UC Clone 56; prostate tissue; diagnosis; immunoassay;  
XX metastatic prostate disease; expression; metastatic prostate cancer;  
XX down regulated; biomarker; benign prostatic hyperplasia; BPH;  
XX non-metastatic prostate cancer; ss.

OS Homo sapiens.

PN WO937811-A1.

PD 29-JUL-1999.

PF 19-JAN-1999; 99WO-US01103.





CC This sequence represents a human cyokeratin 15 cDNA clone isolated  
 CC from a prostate enriched cDNA library. The cyokeratin 15 gene,  
 CC along with the prostate specific transglutaminase (AAH10425) and  
 CC semenogelin II (AAH10427) genes, was found to be specifically expressed  
 CC in prostate tissue, as determined by Southern differential hybridisation  
 CC and relative quantitative reverse transcriptase PCR (RT-PCR). Relative  
 CC quantitative RT-PCR also indicated that prostate specific  
 CC transglutaminase and cyokeratin 15 gene expression is downregulated in  
 CC metastatic prostate cancer tissues compared with normal or benign  
 CC prostate hyperplasia (BPH) prostate tissue. These genes may therefore be  
 CC used as markers for the detection of malignant prostate cells. Although  
 CC semenogelin II was not differentially regulated in malignant prostate  
 CC tissue compared with normal prostate tissue, it was found that  
 CC expression of this gene is downregulated in the blood of patients with  
 CC metastatic prostate cancer compared with normal men, making it  
 CC potentially useful as a diagnostic marker as it can be easily obtained  
 CC from peripheral blood.

SQ Sequence 1709 BP; 389 A; 428 C; 539 G; 353 T; 0 other;

Query Match 7.6%; Score 35.2; DB 21; Length 1709;  
 Best Local Similarity 53.7%; Pred. No. 1.5;  
 Matches 73; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

Qy 322 ctgtgtcctatgtatctacgcagacacagcaggaacttgaaagcgtctcaacacac 381  
 Db 548 ctccggagacagatcatgtccaccacacatcgacacccgtccttgagatcgac 607  
 Qy 382 acctcatccagcgtcagcagcaagcgacatgtgaggaactgttctgcccgaagcc 441  
 Db 608 aatgcgcagcgtcgtcgtcgagcagacttcaggtcagatgatgatgtgctgcctgcgc 667  
 Qy 442 agcggctgtaagccg 457  
 Db 668 cagggcgctgtaggctg 683

## RESULT 24

AAH21845  
 ID AAH21845 standard; DNA: 2822 BP.

XX AAH21845;

DT 15-AUG-2001 (first entry)

XX Rhodococcus sp. amidase encoding DNA SEQ ID NO:6.

XX Rhodococcus. nitrilase; nitrile hydratase beta subunit; amidase;  
 KW nitrile hydratase alpha subunit; carboxylic acid; cyanocarboxylic acid;  
 KW pharmaceutical; agricultural drug; dye; ds.

XX Rhodococcus sp.

XX Key Location/Qualifiers  
 FT CDS 1094..2491  
 FT /\*tag= a  
 FT /product= "amidase"

PN MO200130994-A1.

XX 03-MAY-2001.

PF 25-OCT-2000; 2000MO-JP07464.

PR 26-OCT-1999; 99JP-0303212.

PR 26-JAN-2000; 2000JP-0021797.

PR 10-APR-2000; 2000JP-0107855.

XX (SHOW ) SHOMA DENKO KK.

XX Aoki H, Kamachi H;

DR WPI: 2001-308634/32.

DR P-PSDB: AAB98070.

XX Producing carboxylic acids using Rhodococcus to convert cyano groups of  
 PT nitrile compounds to carboxyl groups

PS Claim 29; Page 75-80; 89pp; Japanese.

XX The present invention describes a method for producing carboxylic acids,  
 CC comprising using a microorganism, whose ability to convert cyano groups  
 CC to amide groups has been removed or reduced, to convert at least one  
 CC cyano group of a nitrile compound to a carboxyl group. Also described  
 CC are: (1) a microorganism for use in the novel method; (2) a plasmid  
 CC containing DNA for Rhodococcus nitrilase gene; (3) a host transformed by  
 CC the plasmid of (2); (4) a nitrilase gene, comprising a 1531 base pair  
 CC sequence (AAH21843), and encoding a 366 residue amino acid sequence  
 CC (AAB98067); (5) producing nitrilase, comprising culturing the host of  
 CC (3) under expression conditions, and recovering the polypeptide; (6) a  
 CC nitrile hydratase gene, comprising a 2822 base pair sequence (AAH21844),  
 CC encoding a 229 nitrile hydratase beta subunit (AAB98068) and a nitrile  
 CC hydratase alpha subunit (AAB98069); (7) producing amides using hosts  
 CC transformed by a 2822 base pair sequence (AAH21845), encoding for  
 CC Rhodococcus amidase (AAB98070). The method can be used for producing  
 CC carboxylic acids and cyanocarboxylic acids which are useful in  
 CC pharmaceuticals, agricultural drugs, dyes and as starting materials for  
 CC other chemicals.

SQ Sequence 2822 BP; 478 A; 1034 C; 869 G; 438 T; 3 other;

Query Match 7.6%; Score 35.2; DB 22; Length 2822;  
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 Db 1234 cctctcagagcagcagccgcgcgcagcctcagcgtcagctcactcaccacagcgga 1293  
 Qy 351 ggagaacttgaaagcgtctcacaacatccacactccatccagctgacgagcaagcgga 410  
 Db 1294 cgagaacccgctgagcgtcgtgtactacacacccatcgatcgagaaaccgagagcc 1353  
 Qy 411 catgtgtggaagactgttctggtccgagcgaagcggtgtgtaagccgg 458  
 Db 1354 cctgcgcggcggaagcgtcgccgtgaaagacacgctcgagtcgccc 1401

## RESULT 25

AAAT45098/C  
 ID AAAT45098 standard; CDNA to mRNA; 2057 BP.

XX AAAT45098;

DT 14-AUG-1997 (first entry)

XX Cytomegalovirus polypeptide encoding cDNA from the antisense RNA.

KW CMV; latency-associated polypeptide; CMV latent transcript; CLV;  
 KW antibody; human; ds.

XX Human cytomegalovirus.

XX

XX

XX

XX

XX

XX

Key Location/Qualifiers

FT CDS 87..266

FT /\*tag= a

FT /note= "Antisense ORF 1"

FT 1081..1545

FT /\*tag= b

FT /note= "Antisense ORF 2"

FT 1106..1240

FT /\*tag= c

FT /note= "Antisense ORF 3"

FT 1524..1982

FT CDS





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OY 211 aatccgcctcctgattgcagcttaacagatgcga 245  
DB 408 ctctcgtatcctctcgaacgagcagcagcttgcga 442  
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18-OCT-2000 (first entry)  
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Hybridisation assay; genetic mapping; gene expression control;  
protein identification; signal transduction pathway; metabolic;  
pathway; promoter; termination sequence; corn; ss.  
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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: January 29, 2002, 15:37:41 ; Search time 1586.09 Seconds

(Without alignments)  
4836.540 Million cell updates/sec

Title: US-09-722-838-1

Perfect score: 465  
Sequence: 1 atggcgctgcgcgcgcgtgt.....gtgctaagccgctaataag 465

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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31: em\_htg\_inv: \*  
32: em\_htg\_rod: \*  
33: em\_htg\_hum: \*  
34: em\_htg\_inv: \*  
35: em\_htg\_rod: \*  
36: em\_htg\_other: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	67	14.4	696	8	CNS019LK	AL11792 Botrytis
2	66.4	14.3	576	8	CNS01DE7	AL116747 Botrytis
3	66.4	14.3	600	8	CNS01AJK	AL113016 Botrytis
4	66.4	14.3	660	8	CNS01ABA	AL112718 Botrytis
5	66.4	14.3	660	8	CNS01AIT	AL112961 Botrytis
6	66.4	14.3	660	8	CNS01ASW	AL113352 Botrytis
7	66.4	14.3	696	8	CNS01A65	AL112533 Botrytis
8	66.4	14.3	720	8	CNS019ZA	AL112286 Botrytis
9	59.8	12.9	481	8	AF399639	AF399639 Picchia an
10	58.8	12.6	540	8	CNS01918	AL11672 Botrytis
11	48.4	10.4	1184	8	SCCOP1	Z14971 S.cerevisia
12	48.4	10.4	1194	8	SCYLL050C	Z73155 S.cerevisia
13	48.4	10.4	2005	8	YSCCOF	D13230 Saccharomyc
14	48.4	10.4	37396	8	SCCH31LST	Z47973 S.cerevisia
15	47.8	10.3	720	8	CNS01DPH	AL117117 Botrytis
16	46.4	10.0	432	8	AB052106	AB052106 Zygosacch
17	42.2	9.1	3615	2	AC014144	AC014144 Drosophila
18	42.2	9.1	133250	3	AC008332	AC008332 Drosophila
19	42.2	9.1	190302	3	AC009352	AC009352 Drosophila
20	42.2	9.1	253648	3	AE003638	AE003638 Drosophila
21	41.2	8.9	189070	2	AC083942	AC083942 Oryza sat
22	39.8	8.6	671	3	ACACTPH	M93361 Acanthamoeb
23	39.8	8.6	11856	1	AE007266	AE007266 Sinorhizo
24	39.6	8.5	908	8	AF032974	AF032974 Oryza sat
25	39.6	8.5	142268	8	AP003018	AP003018 Oryza sat
26	39.6	8.5	159749	8	AP003020	AP003020 Oryza sat
27	39.4	8.5	4807	9	AB011092	AB011092 Homo sapi
28	39.4	8.5	4985	9	AF036927	AF036927 Homo sapi
29	39.4	8.5	5472	9	HSAL33123	AJ133123 Homo sapi
30	39.4	8.5	5515	6	ARI37985	ARI37985 Sequence
31	39.4	8.5	5515	6	AX138768	AX138768 Sequence
32	39.4	8.5	148427	2	AC018981	AC018981 Homo sapi
33	39.4	8.5	299350	1	SME591786	AL591786 Sinorhizo
34	39.4	8.4	133387	2	AP004061	AP004061 Oryza sat
35	38.8	8.3	2674	8	EN037803	U37803 Emeritella
36	38.4	8.3	5998	1	AB032524	AB032524 Streptomy
37	37.8	8.1	4511	9	Y02848511	AY0284859 Homo sapi
38	37.8	8.1	165196	9	AC007151	AC007151 Homo sapi
39	37.8	8.1	215441	9	AC005736	AC005736 Homo sapi
40	37.6	8.1	346897	1	AP002995	AP002995 Mesorhizo
41	37.4	8.0	836	3	GALSERI	L41640 Gallieria me
42	37.4	8.0	39531	1	SCP8	AL1390975 Streptomy
43	37.2	8.0	1845	8	TE14BG	X60652 T. longibrac
44	37.2	8.0	2051	3	AB003034	AB003034 Asterina
45	37.2	8.0	7921	3	AF153362	AF153362 Dictyoste

#### ALIGNMENTS

RESULT 1  
CNS019LK 696 bp mRNA 02-SEP-1999  
LOCUS Botrytis cinerea strain T4 cDNA library under conditions of  
DEFINITION nitrogen deprivation.  
ACCESSION AL11792.1 GI:5826411  
VERSION AL11792  
KEYWORDS cDNA library; nitrogen deprivation.  
SOURCE Botryotinia fuckeliana.  
ORGANISM Botryotinia fuckeliana  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;  
Helotiales; Sclerotiniaceae; Botryotinia.  
REFERENCE 1 (bases 1 to 696)  
AUTHORS Bitton,F., Lewis,C., Fortini,D., Pradier,J.M. and Brygoo,Y.  
TITLE Direct Submission  
JOURNAL Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr,  
78026 Versailles, France  
REFERENCE 2 (bases 1 to 696)  
AUTHORS Genoscope.  
TITLE Direct Submission

JOURNAL Submitted (01-Sep-1997) 00000000-

CP 5/06 91057 EVRY CEDEX - FRANCE (E-Mail: [evry@ceped.fr](mailto:evry@ceped.fr))

RESULT	5				
CNS01A11					
LOCUS					
DEFINITION	CNS01A11	660 bp	mRNA	PLN	02-SEP-1999
ACCESSION	Botrytis cinerea strain T4				CDNA library under conditions of
VERSION	AI112961				nitrogen deprivation.
KEYWORDS	AI112961.1	GI:5827580			
SOURCE	CDNA library;	nitrogen deprivation.			
ORGANISM	Botryotinia fuckelliana.				
	Botryotinia fuckelliana				
	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;				
	Helotiales; Sclerotiniaceae; Botryotinia.				
REFERENCE	1 (bases 1 to 660)				
AUTHORS	Bilton,F., Lewis,C., Fortini,D., Pradler,J.M. and Brygoo,Y.				
TITLE	Direct Submission				
JOURNAL	Submitted (01-SEP-1999)	Phytopathologie, INRA,			route de St Cyr,
	78026 Versailles, France				
REFERENCE	2 (bases 1 to 660)				
AUTHORS	Genoscope.				
TITLE	Direct Submission				
JOURNAL	Submitted (01-SEP-1999)	Genoscope - Centre National de Sequencage :			
	CP 5706 91057 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)				
COMMENT	- Web : www.genoscope.cns.fr)				
	The cDNA library to be analysed within the framework of this				







Query Match	10.48;	Score 48.4;	DB 8;	Length 1184;
Best Local Similarity	57.18;	Pred. No. 0.11;		
Matches 88; Conservative	0;	Mismatches 66;	Indels 0;	Gaps 0;

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Db 822 ATCTCCAAGATGCTTAAAGAGAGCCTTAAC 855

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes  
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

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Matches 88;	Conservative 0;	Mismatches 66;	Indels 0;	Gaps 0

RESULT	13
YSCOF	

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes  
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

Kazuko Iida  
The Tokyo Metropolitan Institute of  
Education

Medical Science  
3-18-22 Honkomagome, Bunkyo-ku  
Tokyo 113

FEATURES	
source	
Phone:	03-3823-2101 x5202
Email:	lidaer@insoken.or.jp
Fax:	03-5685-2932.
	location/Qualifiers
	1. 2005









[illegible]

Gy	200			
Db	97818	AGCACAA	97824	
RESULT	19			
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DEFINITION	Drosophila melanogaster, chromosome 2L, region 34A-34A, BAC clone BACR1M13, complete sequence.			
ACCESSION	AC009352			
VERSION	AC009352.4	GI:13270550		
KEYWORDS	HTG.			
SOURCE	fruit fly.			
ORGANISM	Drosophila melanogaster			
REFERENCE	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephyridroidea; Drosophilidae; Drosophila.			
REFERENCE	1 (bases 1 to 190302)			
AUTHORS	Celniker,S.E., Adams,M.D., Kronmiller,B., Tyler,D., Wan,K.H., Holt,R.A., Evans,C.A., Gocayne,J.D., Amaratilake,P.G., Brandon,R.C., Rogers,Y., An,H.Y., Baldwin,D., Banazon,J., Beeson,K.Y., Busam,D.A., Carlson,J.W., Center,A., Champs,M., Davenport,L.B., Dietz,S.M., Dodson,K.J., Dorsett,V., Doup,L.E., Doyle,C., Dresnek,D., Farfan,D., Gonzalez,S., Ferise,E., Galle,R.F., Garg,N.S., George,R.A., Gonzales,M., Houck,J., Hoskins,R.A., Hostlin,D., Howland,T.J., Idagwem,C., Jalali,M., Kruse,D., Li,P., Mattei,B., Moshrefi,A., McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunoo,J., Pacleb,J., Paragas,V., Park,S., Patel,S., Pfeiffer,B., Phuenaneavong,S., Pittman,G.S., Putl,V., Richards,S., Scheeler,F., Striplston,M., Strong,R., Svirskaas,R., Tector,C., Williams,S.M., Zaveri,J.S., Smith,H.O., Rubin,G.M. and Venter,J.C.			
TITLE	Sequencing of Drosophila chromosome 2L, region 34A-34A			
JOURNAL	Unpublished			
REFERENCE	2 (bases 1 to 190302)			
AUTHORS	Celniker,S.E., Agbayani,A., Arcana,T.T., Baxter,E., Blazek,R.G., Buchenoff,C., Champs,M., Chavez,C., Chew,M., Ciesiolka,L., Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L., Hoskins,R.A., Houston,K.A., Hummelst,S.R., Katta,K., Kearney,L., Kim,E., Lee,B., Lewis,S., Li,P., Lomoton,M.A., Mazda,P., Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S., Pfeiffer,B., Poon,L., Sequiera,A., Sethi,H., Snit,E., Svirskaas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and Rubin,G.M.			
TITLE	Direct Submission			
JOURNAL	Submitted (17-AUG-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA			
COMMENT	On Mar 10, 2001 this sequence version replaced gi:6957892. Sequence submitted by: Berkeley Drosophila Genome Project Lawrence Berkeley National Laboratory, MS 64-121 Berkeley, CA 94720  This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site ( <a href="http://www.fruitfly.org/sequence/">http://www.fruitfly.org/sequence/</a> ) or send email to <a href="mailto:bdg@fruitfly.berkeley.edu">bdg@fruitfly.berkeley.edu</a> .  Location/Qualifiers 1. 190302 /organism="Drosophila melanogaster" /strain="Y: cn bw sp" /db_xref="taxon:7227" /chromosome="2L" /map="34A-34A" /cclone="BACR1M13 (D866)" /clone_id="RPCI-98 (Roswell) Park Cancer Institute Drosophila melanogaster BAC library, partial EcoRI in PBACE3.6")"			
FEATURES				
SOURCE				
BASE COUNT	55642 a 39660 c 39464 g 55536 t			
ORIGIN				



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Db 100284 CCATTAAGGCAACGACACACATCCACAACTAGACGACGACAAAGAAAGAAAAGTTCT 100343

Oy 140 accaggtctcgaagaagactcagaggtcttcgtacaggtcgaaggtcaccagg 199
Db 100344 ACGATGAGGATGACATCATGAGGCGCGGAGGAAAAGCACAGCGCGGATTCGAGGTCCAGGA 100403

Oy 200 atagcaa 206
Db 100404 AGCACAA 100410

RESULT 21
AC083942
LOCUS AC083942 189070 bp DNA HTG 26-MAY-2001
DEFINITION Oryza sativa clone OSJNBa0002D01, *** SEQUENCING IN PROGRESS ***, 5
AC083942
VERSION AC083942.7 GI:14209712
KEYWORDS HTG; HTGS; PHASE1.
SOURCE Oryza sativa.
ORGANISM Oryza sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehhardtidae; Oryzaceae; Oryza.
1 (bases 1 to 189070)
REFERENCE 1
AUTHORS McComble,W.R.
TITLE Rice genomic sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 189070)
AUTHORS McComble,W.R.
TITLE Direct Submission
COMMENT Submitted (07-OCT-2000) Lita Annenberg Hazen Genome Center, Cold
Spring Harbor Laboratories, 1, Bungtown Road, Cold Spring Harbor,
NY 11724, USA
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 73964 73963: contig of 73963 bp in length
* 73964 74922: gap of unknown length
* 74923 118649: contig of 43727 bp in length
* 118650 119607: gap of unknown length
* 119608 146966: contig of 27359 bp in length
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Best Local Similarity 53.0%; Pred. No. 7;
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Db 59997 GGGCCACCAAGAGAGCTTTTCCGCCAGGAGATGGCCGAGACGACGACGACCCCAAGG 600556

Qy 138 CGACGAGTCTCGCAAGAGAGGAGTCTTCCTCGTAGCGAGTCTGAGGTCTACCA 197

Db 60057 GATCCCCCTCCCTCAAGGAGGGAATAATCGTCGGTTCCGCTCCAGCCCGGCCCTGCGC 60118

Qy 198 GGAATGCAAGAGTAACTCCGCTCTCGTATGCAATGCTCTAAGATCTC 243

Db 60117 GAATCGAAGCGGCGCTGCTCTCAGGTGATGTCAATGACAGGCGCTC 60162

RESULT	22				
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LOCUS	Acanthamoeba castellanii		actophorin mRNA, complete cds.		
DEFINITION					
ACCESSION	M93361				
VERSION	M93361.1	GI:155620			
KEYWORDS	actophorin.				
CROSS-REFERENCE	Acanthamoeba castellanii cDNA to mRNA.				
SOURCE	Acanthamoeba castellanii				
ORGANISM	Eukaryota; Acanthamoebidae; Acanthamoeba.				
REFERENCE	1 (bases 1 to 671)				
AUTHORS	Quirk,S., MacIver,S.R., Ampe,C., Doberstein,S.K., Kaiser,D.A.				
TITLE	VanDamme,J., Vandekeckhove,J.S. and Poliard,F.D.				
JOURNAL	Primary structure of and studies on Acanthamoeba actophorin				
MEDLINE	Biochemistry 32 (33), 8545-8533 (1993)				
FEATURES	93363583				
source	Location/Qualifiers				
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	Location= "Acanthamoeba castellanii"				

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BASE COUNT	173 a 213 c 144 g 141 t	
ORIGIN		

Query Match	8.6%	Score 39.8;	DB 3;	Length 671;
Best Local Similarity	56.5%;	Pred. No. 14;		
Matches 74;	Conservative	0;	Mismatches 57;	Indels 0;
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QY	302	ttccctcagacacactactctctgctgctcgtactacgcgcagccacagggagaacttga	361
Db	288	ctcccgactctgcgcccccattcaagtccaaagtatgtaacaccttcacaaagagctccatca	347
QY	362	agaacgctctc	372
Db	348	agaaagacgtc	358

RESULT	23	
AE007266/c		15-AUG-2001
LOCUS	AE007266	11856 bp
DEFINITION	Sinorhizobium meliloti plasmid pSymA section 72 of 121 of the complete plasmid sequence.	
ACCESSION	AE007266	AE006469
VERSION	AE007266.1	GI:14523915
KEYWORDS	Sinorhizobium meliloti.	
SOURCE		

	ORGANISM
JOURNAL PUBLISHED REFERENCE AUTHORS	Sinorhizobium meliloti Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group. Rhizobiaceae; Sinorhizobium.
TITLE	1 (bases 1 to 11856) 2 (bases 1 to 11856)
JOURNAL PUBLISHED REFERENCE	Barnett,M.J., Fisher,R.F., Jones,T., Komp,C., Abola,A.P., Barloy-Hubler,F., Bowser,L., Capela,D., Galibert,F., Gouzy,J., Gurjal,M., Hong,A., Huizer,L., Hyman,R.W., Kahn,D., Kahn,M.L., Kalmann,S., Keating,D.H., Palm,C., Peck,M.C., Surzycki,R., Wells,D.H., Yeh,K.-C., Davis,R.W., Federspiel,N.A. and Long,S.R. Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti pSMA megaplasmid Proc. Natl. Acad. Sci. U.S.A. 98 (17), 9883-9888 (2001)
AUTHORS	1 (bases 1 to 11856) 2 (bases 1 to 11856)
TITLE	Barnett,M.J., Fisher,R.F., Jones,T., Komp,C., Abola,A.P., Barloy-Hubler,F., Bowser,L., Capela,D., Galibert,F., Gouzy,J., Gurjal,M., Hong,A., Huizer,L., Hyman,R.W., Kahn,D., Kahn,M.L., Kalmann,S., Keating,D.H., Palm,C., Peck,M.C., Surzycki,R., Wells,D.H., Yeh,K.-C., Davis,R.W., Federspiel,N.A. and Long,S.R.
JOURNAL PUBLISHED REFERENCE	Submitted (29-MAR-2001) Biological Sciences, Stanford University Directed Submission Location/Organism
AUTHORS	371 Serra Mall, Stanford, CA 94305, USA

FEATURES	SOURCE
TITLE	Direct Submission
JOURNML	Submitted (29-MAR-2001) Biological Sciences, Stanford University 371 Serra Mall, Stanford, CA 94305, USA
	Location/Qualifiers
	1. 11856
	/organism="Sinorhizobium meliloti"
	/strain="1021"
	/db_xref="taxon:382"
	/plasmid="pSymA"
gene	complement(116. .1468)
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	complement(116. .1468)
CDS	/gene="Sma1447"

gene  
CDS

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/ gene="Sma1447"
/ note="glimmer prediction; global similarity to Benk, a
benzoate transport protein in P. putida; pfam domain
homology to sugar and other transporters"
/ codon_start=1
/ trans1_table=1
/ product="putative transmembrane transport protein"
/ protein_id="AAK65448.1"
/ db_xref="gi:14523916"
/ translation="MLINAAARQLEKGRMTITVDDALDPAAGCTGYORLMAIFGLVMA
ADAMOVAVGFTFAASIAATFGLIVPAOLQGTGLTFEGLMFGAAGPFRIADIRGRRLV
IATVCAVADFGLLSYFAQDFVLLRLRELTGAAGVGLPVDVAMAEFLPARRGVLL
VLMEEFPAAVGLITVLAAMASLAGVADAMRYIFVPAVPAIALLGLVLRLEPSPILY
LNRGTSSEAKAIVDEIIVVNGMRKRGAGSLVPEPPASGISADLRKRSWILAIW
FLVLSIYGVATFMPRLPAGSGRGFRGVGLVYLAALQIPGALAAVGEKGRPT
LIGFCLLSALGCLTFVAAQTMLIGVSLIIMSFALIGTWCALVATPELPTSRVATG
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complement(1918..3108)
/ gene="Sma1450"
/ complement(1918..3108)
/ gene="Sma1450"
/ function="Small molecule metabolism"
/ note="glimmer prediction; global similarity to PhaA, a
thiolase from P. putida (gi:1857942); global similarity
to acetyl-CoA acetyltransferase from C. acetobutylicum and
A. eutrophus (gi:1174677); pfam domain homology to
thiolase"
/ codon_start=1
/ trans1_table=1
/ product="Probable thiolase"
/ protein_id="AAK65449.1"
/ db_xref="gi:14523917"
/ translation="MNKODPVVIVGOAPRPLGSGFOGELKDSADLGAATVDALKRR
GLADVADYVRFQVITLGGOGAPARQALAGLIPGVGATVYVNGKSGKAAVLAHGR
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MGSEFDECAEAYOFTRSAODERYIASLEFAOKRASADGSEAFETVPLSTASGKEGTVA
IDVEOPKARLDKTIPLKPAFRDGGTITAAANSISDGAALVIMRSAADKOGIPLTVA
VIGCATHADAPSLFPAPIGAIKALCIRGMDIGVDVLEFENEAPAVPMAAMBEIG
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complement(3133..3900)
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CDS      /gene="Sma1452"
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          similarity to short chain"
          /codon_start=1
          /transl_table=11
          /product="Probable"
          /protein_id="AAK65450.1"
          /db_xref="GI:14523918"
          /translation="MOLKSRVITYTGSSSGAAYTMTAQEGATVGLDKPRAGE
          PAELGAAVFRNADVTNEDATRALAFKOEFGHVGILVNCAGTAPERGEITLRSRGP
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          RLGRAEEYALVHICENTMLNGEVIRLDGALRMAR"
          3995. .5065
          /gene="Sma1454"
          3995. .5065
          /function="Miscellaneous; Not classified regulator"
          /note="glimmer prediction; global similarity to Ocr from
          P. aeruginosa (GI: 1657970) which regulates ornithine
          utilization; Pfam domain similarity to N-terminal
          helix-turn-helix motif"
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          /db_xref="GI:14523919"
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          RHAPANILVVRHHDAGLSAIRORLHATAPAMPGEPAIAARRIAPTLRRLRQSG
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          SGRLPKDOLSMG"
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          /note="glimmer prediction"
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/gene="Sma1461"
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          /function="Small molecule metabolism; Central intermediary
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          /note="glimmer prediction; global similarity to muconate
          cyclisomerase in P. putida (GI: 77758); Pfam domain
          similarity to mandelate racemase / muconate lactonizing
          enzyme family"
          /codon_start=1
          /transl_table=11
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          /protein_id="AAK65455.1"
          /db_xref="GI:14523923"
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          ERFVYLVKGGEKIDLEITAAVREIGEDALRLDANGVSHVAINCRKLEKYDIEF
          IEQPTVMSIPMAHVRKVGIPVADQAFTLYDVYIEORADAMICIGPREIGCI
          OPMKAAVAAGAEALKICISHSFTGTTCAEHHIGALRNLDGQNMIMQVOEDIV
          SPDLPRTKNMADLFRKRGIGFOLAEDELVAEGSERVAAS"
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          complement(8311. .9201)
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          /function="Cell processes; Transport of small molecules"
          /note="glimmer prediction; global similarity to
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          (GI:7404430) and several putative ABC transporter
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          the choline transport system"

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Query Match      8.6%: Score 39.8; DB 1; Length 11856;
Best Local Similarity 47.7%: Pred. No. 15;
Matches 116; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

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QY	186	CGAGGCTACCAAGATAGCAAGGTAATCCGCTCCGCTATGCAAGTCTAGTCTGA	245
DB	7756	CGAAGCCGCGAGAGAGCTGGCGCGGATGCGCGCTGCGCACCGCCGAGCGGCGGT	7697
QY	246	gtacgattcgglygcygltgaggaagaagaagaatgtttcatctctcgggtcc	305
DB	7696	CTTCTATCTCAAGGTGCGCGCGGAGAAACTCGACTCGAGATACACCGCGGCGGTTCG	7637
QY	306	ctcagacacactactctgtgtgltccatgattcagccagacacagggaacattgaaagaa	365
DB	7636	CGGCGAGATCGCGCATGGCGCGCTTCGCTCGATGCGCAACCAAGCGTGGACCGCTCATGA	7577
QY	366	cgctctcaacatccacaccctccatccacgcgcgagcaagggcgacattgaggaagac	425
DB	7576	CGGCATCAACTGTGCGCGCAAGCTCGAATAATACGACATCGAATTTCATTGACGACCGGAC	7517
QY	426	tgt 428	
DB	7516	CGT 7514	

RESULT 24	AF032974	908 bp	mrna	PLN	03-MAR-1998
LOCUS	AF032974	908 bp	mrna	PLN	03-MAR-1998
DEFINITION	Oriza sativa germin-like protein 4 (GER4) mRNA, complete cds.				
ACCESSION	AF032974				
VERSION	AF032974.1	GI:2655290			
KEYWORDS					
SOURCE	Oriza sativa.				
ORGANISM	Oriza sativa				
REFERENCE	Oriza sativa				
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
TITLE	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;				
JOURNAL	1 (bases 1 to 908)				
REFERENCE	2 (bases 1 to 908)				
AUTHORS	Member, N. and Bernier, F.				
TITLE	The rice genome expresses at least six different genes for oxalate				
JOURNAL	oxalate/germin-like proteins (Accession Nos. AF032971, AF032972,				
FEATURES	AF032973, AF032974, AF032975, and AF032976) (PCR98-021)				
source	Plant Physiol. 116 (2), 868 (1998)				
Location/Qualifiers	1..908				
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CDS	/strain="Nipponbare"				
	/db_xref="taxon:4530"				
	/clone="Rice Genome project clone RICS0890A"				
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	54..704				
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	/note="similar to wheat and barley oxalate oxidase"				
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	/protein_id="AAC04835.1"				
	/db_xref="GI:2655291"				
	/translation="MARVOLWVAACAVLALALAPSLAGDPMLODCVADLASPKYK				
	NGPCKANVTADDFPAGLKNQNTNPNPAGSVNTANVOSFPGVTLVSMKIDYIA				
	GGNPFRPHIRPRATEIFIVLEGLVEGFIITANKLETKVTAGAEVFPFGLVHFCQNN				
	GGHAAVIAFNSQLOGTQAIATITLPAAPVPVPSDLAKAFRVDVPAQDAIKAKK"				
	908				
	/gene="GER4"				
BASE COUNT	164 a	298 c	253 g	193 t	
ORIGIN					
Query Match	8.5%;	Score 39.6;	DB 8;	Length 908;	
Best Local Similarity	57.1%;	Pred. No. 16;			
Matches 72;	Conservative 0;	Mismatches 54;	Indels 0;	Gaps 0	
QY	137 tcgacagagctcgcgaagaagagactcgaagcttccttcgtagcagagctcgagctacaa	196			
Db	517 tgcagcagagccgcgcggagcgaagaccctcgccgcgggagacagcttctgtaaacagc	458			
QY	197 aggatagcgaaggtatataccgctcctgttagtcagttcagatcgcagtagcagctcg	256			
Db	457 ttgtttggcgcgtgtatgaagccaccttcgagagagcgcctcgagagacgaaagatgattcgc	398			
QY	257 gtcgcg 262				
Db	397 gtgcgcg 392				
RESULT 25	AP003018	142268 bp	DNA	PLN	29-MAR-2001
LOCUS	AP003018	142268 bp	DNA	PLN	29-MAR-2001
DEFINITION	Oriza sativa genomic DNA, chromosome 1, BAC clone:OSNBB0004B13.				
ACCESSION	AP003018				
VERSION	AP003018.2	GI:13486711			
KEYWORDS					

SOURCE ORGANISM	REFERENCE AUTHORS	JOURNAL TITLE	REFERENCE AUTHORS	JOURNAL TITLE	COMMENT
<i>Oryza sativa</i> (cultivar: Nipponbare); <i>Zm</i>					
<i>Oryza sativa</i>					
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;					
Ehrhartoideae; Oryzaceae; <i>Oryza</i>					
1 (sites)					
Sasaki,T., Matsumoto,T. and Yamamoto,K.					
<i>Oryza sativa</i> nipponbare(Gs3) genomic DNA, chromosome 1, BAC					
clone:OSUNba0004B13					
Published Only in Database (2000) In press					
2 (bases 1 to 142268)					
Sasaki,T., Matsumoto,T. and Yamamoto,K.					
Direct Submission					
Submitted (06-DEC-2000) Takuji Sasaki, National Institute of					
Agrobiological Resources, Rice Genome Research Program, Kannondai					
2-1-2, Tsukuba, Ibaraki 305-8602, Japan					
(E-mail:tsasaki@agr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/					
tel:81-298-38-7441, Fax:81-298-38-7468)					
On Mar 28, 2001 this sequence version replaced g1:11602825					
Genes were predicted from the integrated results of the following:					

Oryza sativa (cultivar:Nipponbare) DNA, clone:OSJNBa0004B13.  
Oryza sativa  
Eurycotyca; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Pernambuco; Magnoliopsida; Liliopsida; Poales; Poaceae;  
Eriocaulaceae; Oryzaceae; Oryza.  
1 (sites)  
Matsumoto,T. and Yamamoto,K.  
Oryza sativa nippobare(GA3) genomic DNA, chromosome 1, BAC  
clone:OSJNBa0004B13  
published Only in Database (2000) In press  
2 (bases 1 to 142268)  
Sasaki,T., Matsumoto,T. and Yamamoto,K.  
Direct Submission  
Submitted (06-DIC-2000) Takuji Sasaki, National Institute of  
Agrobiological Resources, Rice Genome Research Program, Kannondai  
2-1-2, Tsukuba, Ibaraki 305-8602, Japan  
(E-mail:tsasakite@affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/  
Tel:81-298-38-7441, Fax:81-298-38-7468)  
On Mar 28, 2001 this sequence version replaced gi:1160282.  
Genes were predicted from the integrated results of the following:  
GENSCANL.0, BLASTN2.0, BLASTX2.0 as well as SplicePredictor  
(October 1998 version). The genomic sequence was searched against  
NCBI Nonredundant Protein database, nr  
(ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at  
RGP. Protein homologues of the coding regions were searched against  
NCBI Nonredundant Protein database with BLASTP2.0. ESTs represent  
the identified cDNA sequences using RGP clone ID.  
corresponding DBU accession no. and RGP clone ID.  
A gene with identity or significant homology to a protein is  
classified based on the protein name to indicate the homology level  
such as same name, 'putative-' and '-like protein'. A gene without  
significant homology to any protein but with EST homology (covering  
almost the entire length of partial sequence) is classified as an  
'unknown' protein. A gene predicted with a gene prediction program  
is classified as a 'hypothetical' protein.  
The orientation of the sequence is from -21M13 to M13rev of the BAC  
clone. This sequence of OSJNBa0004B13 clone has an overlap with  
PO498A12 (DBJ: AP003020) clone at the position 59,286 to 142,268  
of 3' end. The sequence of this clone ends at the position 82,983  
of PO498A12. Detailed information on overlap and assembly quality  
together with annotation of this entry is available at  
<http://rgp.dna.affrc.go.jp/Genomeseg.html>.

FEATURES

source

Location=Oxalis stricta  
1..142268  
/organism="Oryza sativa"  
/cultivar="Nippobare"  
/db\_xref="taxon:4530"  
/chromosome="1"  
/clone="OSJNBa0004B13.3"  
complement(join(43..143,495..529,646..686))  
/gene="OSJNBa0004B13.1"  
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note="hypothetical protein"  
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/protein\_id="BAB39947.1"  
/db\_xref="GI:13486712"  
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join(2013..2128,2281..2652,2869..3022)  
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GGPLPWADAGEGERGRDAGCEGRGRDMSACEGRRRGDSAGEERGMGSASVGE  
SASEDEPSHRDASGAPARWTSKRTRIPARSYPVSHAMPREKRREEDBKRR  
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complement(4476..4995)  
/note="3' LTR"

LTR

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SASEDEPSRMASGAAIRGATGSRKRVSPAASPVHSHAPRKRRRRRREDEGK
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complement(4476..4595)
note="3' UTR"

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FGASFTVEYRRKASRLARRLMSPGHRTLVKPSPTNGRIRYHSPSAELLPADEL
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CASWQVGSQMDAMQTDDETCVPDEILQRTSCELHIFKNLSIKTISHYKVASRM
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PPCPAPPTRRSQAASPARRETKAKADATKNEPPYDCSOEELDAVAGEVROL
KRSEPKIPIIDPSVKNFPGKSTNKALQISDVRTLORAYHKKSKIVPOLGQEPN
QVEPLVNGEDGITEFISDGLTYDQNGAPIPRAEYAYFELKNDYFPGNLSGR
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Query Match 8.5%; Score 39.6; DB 8; Length 159749;

Best Local Similarity 57.1%; Pred. No. 17;

Matches 72; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

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QY 137 tcgaagaggtctcgcaagaagagtaagaggtcttcgttagcaggtctgaggtaccca 136
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DB 31726 TGGACACAGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 31785
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 197 aggatagcaaggtatccgcgtcctcgtatcagttcagttcagttcagttcagttc 256
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 31786 TTCTTGCGAGTGTGATGAAGCCACCTCGAGAGAGAGAGAGAGAGAGAGAGATCTCG 31845
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 257 gtggcg 262
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DB 31846 GTGGCG 31851

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RESULT 27  
 AB011092 4807 bp mRNA PRI 10-APR-1998  
 LOCUS Homo sapiens mRNA for KIA0520 protein, partial cds.  
 DEFINITION  
 ACCESSION AB011092

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VERSION
AB011092.1 GI:3043563
KEYWORDS
KIA0520 protein.
SOURCE
Homo sapiens male brain cDNA to mRNA, clone_11b:pbunescriptII SK
plus clone:HG1313.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 4807)
Ohara,O., Nagase,T., and Ishikawa,K.
Direct Submission
Submitted (13-FEB-1998) to the DDBJ/EMBL/Genbank databases. Osamu
Ohara, Kazusa DNA Research Institute, DNA Technology; 1532-3 Yama,
Kisarazu, Chiba 292-0812, Japan (E-mail:cdna@info.kazusa.or.jp,
Tel:+81-438-52-3913, Fax:+81-438-52-3914)
2 (sites)
Nagase,T., Ishikawa,K., Miyajima,N., Tanaka,A., Kotani,H.,
Nomura,N. and Ohara,O.
Prediction of the coding sequences of unidentified human genes. IX.
The complete sequences of 100 new cDNA clones from brain which can
code for large proteins in vitro
DNA Res. 5 (1), 31-39 (1998)
98290545
FEATURES
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SPLDANONFSSEENPCNSSVPRDLRRPASLIGEVVLPFLLLVLPFLNREVEYSR
LHYGVEDVADHRTKQSMRDADMLRNTITPYNVAEOLKYSQTSKKNDSGVITAS
TVNFSFTYENBEGKECYRVNLELIGDEDELISKPDYSIEKTIKGTITMAAGLN
TAOAGSHPQEHQLILFEFAKEMVYVDENNNMLMFKLVGNHPLTAGVGT
TKLYIDMDTVIAISRMDTGVGCRIOVSEESYRVLSMKGYDFRGVNVGKGM
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BASE COUNT 1034 a 1395 c 1241 g 1137 t  
 ORIGIN

Query Match 8.5%; Score 39.4; DB 9; Length 4807;

Best Local Similarity 57.9%; Pred. No. 18;

Matches 70; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

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DB 790 TCCAAGAACACGACACGAGGAGGATCTTCCGCCAGCATTCGACGAGATTC 849
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QY 388 atccagcgtcgaagcaagggcagcatctgagtggaagactctctgcgcagcagcgt 447
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DB 850 TACGAGAGAACTACGAGCGCGCAGAGAGAGAGAGAGAGAGAGAGAGATCTCGG 909
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RESULT 28  
 AF036927 4985 bp mRNA PRI 25-JUN-1998  
 LOCUS AF036927





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